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Minimum |
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ancoding colo	ABK45138	24		34.4	416.8	9	
cDNA encoding colo	ABK44775	24		34.5	418.4	0	
Human ovarian anti	ABQ54923	24		40.8	495	c 7	
Transcription fact	AAT14037	17		96.2	1167	ا ت	
Transcription fact	AAT14038	17		96.5	1170	, UI	
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ES	SUMMARIES						

New nucleic acid encoding human transcription factor IIIA, useful for treatment and diagnosis of cancer and inherited disease $\,$

WPI; 2000-387419/33.

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ALIGNMENTS

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RESULT 1
AAA15407
09-NOV-1999;
                                                                                                                                                                Human; transcription factor; htfIIIA; DNA-binding protein; transcription; ribosomal RNA 5S gene; transcriptional control;
                                                                                                                                                                                                           04-SEP-2000
                                       Bordon-Pallier F,
                                                        (HMRI ) HOECHST MARION ROUSSEL
                                                                       10-NOV-1998;
                                                                                                        18-MAY-2000.
                                                                                                                       WO200028024-A1
                                                                                                                                        Homo sapiens.
                                                                                                                                                                                       Fragment of DNA encoding a transcription factor designated htfIIA.
                                                                                                                                                                                                                           AAA15407;
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                                                                       98FR-0014146.
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Best Local Similarity
Matches 1213; Conserv
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         GACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATG
                                          TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
                                                                                      CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
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llarity 100.0%;
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3; Page 38-39;
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ribosomal RNA 5S gene;
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The cocancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention diagnosis and treatment of diseases associated with inappropriate expression. For example, N and P may be used to treat disorders
                                                                                       Claim 1; Page 3273-3274;
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03-NOV-1999;
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and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                The sequence encodes human transcription factor-IIIA (hTFIIIA),

C a DNA binding protein with 9 zinc finger domains, which is necessary

C for the initiation of 5S RNA gene transcription, binding to an

C internal control region of the 5S gene. A fuller cDNA sequence

with flanking regions is given in AAT14038. A fragment lacking a

5'-portion of the gene has been isolated from a human foetal brain

C cDNA library (OTK7-1), and the 5'-portion of the gene has been

1 solated by 5'-rapid amplification of cDNA ends using primers H11-R

C (AAT14039), H1-E (AAT14040), H1-H (AAT14041) and AP-2 (AAT14042),

C complementary to anchor primer AAT14043. Reverse transcription using

H-11R is followed by anchor primer ligation and PCR using AP-2 and

H1-E, to give a full-length cDNA, OTK7. The gene and its encoded

C protein may be used in diagnosis, identification or therapy of

hereditary diseases such as cancer, or other diseases resulting from

abnormal transcriptional control, and to analyse the mechanisms
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Matches
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                                                                                                                                                                                              Sequence 1269
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP4328) and to cDNAs encoding them (AB054131-AB056305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen CC recombinant vectors and host cells comprising human ovarian antigen CC recombinant vectors and host cells comprising human ovarian antigen CC reating, prognosing or preventing various ovary and/or breast related CC disorders. Such conditions include ovarian cancer and breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and CC disorders (e.g., infertility, disorders of pregnancy, anovulation, cpolycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic cyspiratory cyndrome), inflammatory conditions (e.g., mastitis, oophoritis and cyspinitis), immune disorders (e.g., congenital and acquired ununodeficiencies, autoimmune oophoritis, systemic lipus crythematosus), conditions (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders (ovarian antigen polypeptides and condulate ovarian antigen be used in screening for compounds which condulate ovarian antigen be used in screening for compounds which condulate ovarian antigen polypeptides may for individuals and in forensic analysis, and the dentification of individuals and in forensic analysis, and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
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                    polypeptides may be used as food additives or to prepare antibodies
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  in disease diagnosis,
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31-JUL-2001; 2001WO-US24218
                                                  14-FEB-2002
                                                                                                                                                                                                    immunotherapy;
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                                                                                                                                                                                                 colon tumour;
therapy; gene;
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                                                                                                                                                                                                                                                                                    colon
                                                                                                                                                                                                                                                                              tumour protein,
                                                                                                                                                                                                                                                                                                                                 entry)
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94.8%;
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Pred. No. 2.5e-1
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                                                                                                                                                                                                                               cancer; immunogenic;
                                                                                                                                                                                                                                                                                 SEQ ID
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RESULT 9
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28-MAR-2001;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK44450-ABK46237 represent coding sequences of human colon tumour proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but supplied by the European Patent Office.
                                                                                                                                                     1154
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                                               ABK45138 standard;
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                                                                                                                                                                                                 GGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAACGGAGAG
                                                                                                                                                                                                                                           AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCATCTCAGT 1093
                                                                                                                                                                                                                                                                                                                                                                   CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTTAATCTCCAAAGCCAT 913
                                                                                                                                                                                                                                                                                                       CGCTGTCCAAGAGAAGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419;
                                                                                                                                                                                 ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG 1033
                                                                                                                        TCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAA
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2001US-279763P.
2001US-302051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to polynucleotides encoding colon tumour proteins
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28-MAR-2001; 2001US-279763P
29-JUN-2001; 2001US-302051P
1094
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence date for this patent did not form part of the printed specification supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response against cancer, particularly for the immunotherapy colon cancer, and as markers for the progression of cancer.

ABK4450-ABK46237 represent coding sequences of human colon tumour
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GGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAACGGAGAG
                                                                                                       ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG 1033
                                                                                                                                                                                                              CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCAT 120
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                                                          AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCATCTCAGT 109:
                                                                                       ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG
                                                                                                                                                   al Similarity
418; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                  34.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein,
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                  Score 416.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secrist
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              G; 106 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides, useful as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                                                                                                                                                                                                                                               .7e-101;
                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 10
ABQ59499
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                                                     õ
                                                                            Matches
                                                                                         Query Match
Best Local
                                                                                                                                                   used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1154
                                                                                                                                            antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2000; 2000US-237271P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ59499 standard;
                                                                                                                                                                                                                                                                                      expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                      or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid that is differentially expressed tissues useful for determining the presence of colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-426115/45
                                                                                                                                                                                                                                                                                                                                                                                                                                  Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2001; 2001WO-US30732
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Thiaglingam
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            662
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                                  123
                                                                                       Local
GCCAAGGCCCACGAGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAA 420
                                                     AAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACCCAACTGTGGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAGGTCCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon
                                                                                      Similarity
                                                                                                                     537 BP; 196 A; 116 C; 106 G; 117 T; 2 other;
                                                                                                                                                                                                                                                                                                            to ABQ60787 represent isolated nucleic acids (I) differentially
                                                                                                                                                                                                                                                                                                                                Fig 1; 796pp; English
                                                                                                                                          and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP
                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    er; cancer; tissue profiling; fc
diagnostic; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                      30.8%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                        ME:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence
                                                                            0,
                                                                                    Score 374;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Catino TJ,
                                                                                     DB 24;
                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forensic; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; ss
                                                                                               Length
                                                                           Indels
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n a cell
                                                                          Gaps
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV49231;
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                                                                                                                                                                                                                                (MILL-)
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                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
(d) assessing the efficacy of a therapy
in a patient;(e) selecting a composition for inhibiti
                                                                                                                                                                                                                                                                         Claim 1; Page 9624; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; pharmacogenomic marker; gene; ss.
                                                                            cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                              2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGTGGCAAAACATTTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGTGGCAAAACA-TTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCAAAGCCATATCCTCTCCTTCCATGAGGAAAGCCCGCCTTTTTNGTGTGAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
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inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinogen; pharmacodyanamic marker;
                                              for inhibiting prostate cancer
prostate cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1016
  a patient;
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Best Local Similarity
Matches 302; Conserv
                                                      17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
Novel isolated nucleic acid molecule associated with cancerous prostate cells and correlating with presence of prostate cancer
                                                                                                                                                        Human;
                                                                                                                                                                                 13-SEP-2002
                                                                                                                                                                                             ABV19459
                                                                                                                                                                                                         ABV19459
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                 pharmacogenomic
                                                                                                              23-AUG-2001
                                                                                                 20-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                                                                                            797
                                                                                                                                                                                                                                                                                                                                                                                                                                        assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                   TTT
                                                                                                                                                                                                                                                                     TGTCCAAGAGAAGCTGTGGGAAGAACCTATACTGCTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                              GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA 736
                   2001-662795/76
                                                                                                                                     sapiens
                                                                                                                                                                                                                                        TTT
                                                                                                                                                                                                                                                              TGTCCAAGAGAAGCCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                 prostate cancer; cytostatic;
cogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             also
                                          MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                   979
                                                                                                                                                                                                                                                                                                                                                                                                                 466
                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                        466
                              77
                                                     2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
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                                                                                                 2001WO-US05171
                             Endege
                                                                                     2000US-183319P.
                                                                                                                                                                    expression
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                                                                                                                                                                                                         cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                             as a
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                                                                                                                                                                                                                                                                                                                                                                                              24.8%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacodyanamic or
                               Monahan
                                                                                                                                                                    marker
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                                                                                                                                                                                                                                                                                                                                                                                              Score 301.4;
Pred. No. 1.
                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                          MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                    cDNA 19450
                                                                                                                                                                                                                                                                                                                                                                                                                 ິຍ
                                                                                                                                                       carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                              .4e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                 other;
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useful
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RESULT 13
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(a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                                                                        Human eukaryotic initiation
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RESULT 14
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  31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS73534 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP
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                                                                                                             11-OCT-2001
                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel
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RESULT 15
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 9338; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
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P-PSDB; ABG09347.
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275; Conserv
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95.5%;
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Pred. No. 9
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Search completed: February 10, Job time: 293.158 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46237 represent coding sequences of human colon tumour proteins of the invention.

Note: With the exception of SEQ ID NO 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 234 BP; 83 A; 50 C; 53 G; 48 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding colon tumour protein, SEQ ID No 610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 610; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
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                                                                             GTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATGCCGGGAAAACATTT 793
                                                                                                                          TATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAAACAT 739
                                                                                                                                                                                                                                                         colon tumour;
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ALIGNMENTS

RESULT 1
TF3A_HUMAN STANDARD; PRT; 423 AA.
ID TF3A_HUMAN STANDARD; PRT; 423 AA.
AC Q92664; Q13097; Q12963;
DT Q1-NOV-1997 (Rel. 35, Created)
DT Q1-NOV-1997 (Rel. 35, Last sequence update)
DT Q1-CYT-2001 (Rel. 40, Last annotation update)
DT 16-CYT-2001 (Rel. 40, Last annotation update)
DE Transcription factor IIIA (Factor A) (TFIIIA).

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

GTF3A.

NCBI_TaxID-9606;

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SEQUENCE Fetal brain;
TISSUE-Fetal brain;
MEDLINE-95309028; PubMed-7789179;
MEDLINE-95309028; PubMed-7789179;
Arakawa H., Nagase H., Hayashi N., Ogawa M., Nagata M.,
Fujiwara T., Takahashi E., Shin S., Nakamura Y.;
Fujiwara T., Takahashi E., Shin S., Nakamura Y.;
"Molecular cloning, characterization, and chromosomal mapping novel human gene (GTF3A) that is highly homologous to Xenopus transcription factor IIIA.";
transcription factor IIIA.";
Connect Cell Genet. 70:235-238(1995).
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94342241; PubMed=8063702;
Moorefield B., Roeder R.G.;
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                                                                                                                                                                                                                                                      "Purification and characterization of human
                                                                                                                                                                                                                                                                                                                                      "Cloning and expression Kenopus TFIIIA.";
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EMBL; U20272; AAA75
EMBL; U14134; AAA21
HSSP; P03001; 1TF3.
TRANSFAC; T04953; Genew; HGNC:4662; G
     TF3A_XENLA STANDARD: PRT: 366 AA. P03001; Q91856: 21-JUL-1986 (Rel. 01, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 41, Last annotation update) 16-OCT-2001 (Rel. 41, Last annotation update) 17-2007 (Rel. 41, Last annotation update) 17-2007 (TFIIIA)
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
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 nurtiple internal repeats within the structure of the 5S binding transcription factor TF-IIIA from Xenopus laevis." Studia Biophys. 107:237-247(1985).
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                                X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS)
MEDLINE-98169475; PubMed-9501194;
Nolte R.T., Conlin R.M., Harrison S.C
                                                                         "Domain packing and dynamics zinc fingers of TFIIIA."; Nat. Struct. Biol. 4:605-608(
                                                                                                          Foster M.P., Wuttke D.S., Gottesfeld J.M., Wright P.
                                                                                                                              STRUCTURE BY NMR OF 10-101.
MEDLINE-97397344; PubMed-9253405;
                                                                                                                                                                                                                             consecutive repeats."; FEBS Lett. 186:271-274(1985).
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Kim S.H., Darby M.K., Joho K.E., Brown D.D.;
"The characterization of the TFIIIA synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-26 FROM N.A. MEDLINE-91071587; PubMed-2
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Genes Dev. 3:651-662(1989).
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MEDLINE-85074456; 1
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MEDLINE-85231235;
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       Conlin R.M., Harrison S.C., Brown roles for zinc fingers in DNA recotranscription factor IIIA complex.
transcription factor . Acad. Sci. U.S.A. 9
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the gene for Xenopus transcription
Res. 14:2187-2201(1986).
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cture of transcription
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PubMed=3754326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: ACTS AS BOTH A POSITIVE TRANSCRIPTION FACTOR FOR 5S RNA GENES AND A SPECIFIC RNA BINDING PROTEIN THAT COMPLEXES WITH 5S RNA IN OCCYTES TO FORM THE 7S RIBONUCLEOPROTEIN STORAGE PARTICLE. MAY PLAY AN ESSENTIAL ROLE IN THE DEVELOPMENTAL CHANGE IN 5S RNA GENE EXPRESSION. INTERACTS WITH THE INTERNAL CONTROL REGION (ICR) OF APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED FOR CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III. ALSO BINDS THE TRANSCRIBED 5S RNA'S.

-I- SUBCELLULAR LOCATION: Nuclear.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; S-TFIIIA (IN SOMATIC CELLS) AND O-TFIIIA (IN OCCYTES); ARE PRODUCED BY ALTERNATIVE INITIATION.
-I- TISSUE SPECIFICITY: SYNTHESIZED IN OCCYTES AND, IN WICH LOWER LEVELS, IN SOMATIC CELLS.
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EMBL;
PIR; /
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InterPro; IPR000822; Znf_C2H2.
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L; X03737; CAB51745.1; JOINED.
L; X03737; CAB51745.1; JOINED.
L; X03738; CAB51745.1; JOINED.
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1TF6; 08-JUL-98
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S40785; S40785.
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               ZINC FINGERS.
C2H2-TYPE.
C2H2-TYP
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Best Local Sin
Matches 196;
Interpro: IPR000822; znf_C2H2.

£fam; pF00096; zf-C2H2; 9.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; znf_C2H2; 9.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.
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Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Gonearison of the sequence and structure of transcription fact
IIIA from Bufo americanus and Rana pipiens.";
Gene 120:197-206(1992).
-!- FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR)
APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS RQUIRED
CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III.
BINDS THE TRANSCRIBED 5S RNA'S.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TF3A_RANPI STANDARD; PRT; 335 AA p34695; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation updat Transcription factor IIIA (Factor A) (TFIII
                                                                                                                                                   EMBL; M85211; AAA49534.1; -.
EMBL; X58369; CAA41260.1; -.
PIR; JC1441; JC1441.
HSSP; P03001; ITF3.
                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern leopard Eukaryota; Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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Best Local
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA).
Xenopus borealis (Kenyan clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Verteb
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ZN_FING
                                                                             SEQUENCE FROM N.A.

MEDLINE=90235278; PubMed=2331751;
Joho K.E., Darby M.K., Crawford E.T., E
"A finger protein structurally similar
exclusively to 55 RNA in Xenopus.";
Cell 61:293-300(1990).
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                                                                                                                                                                                                                                                                                MEDLINE-90245658; PubMed-2110661;
Gaskins C.J., Hanas J.S.;
"Sequence variation in transcript
                                                                                                                                                                                                                                    Nucleic Acids
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                            KSKE
                                                                             KRKO
                                                                                                                                                              EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPP
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                                                                                                                                                                                                                                 CHQEPVMCDECKRTFKHKDYLRNHKKTHKKERTVYCCPRDGCERSYTTEFNLQSHMQSFH
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                                                                                                                                 EEQRPFACEHAECGKSFAMKKSLERHSVVHDPEKR---KLKEKCPRPKRSLASRLSGCAPP
                               308
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331

304

246 271

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PROSITE; PSO0028; ZINC_FINGER_C2H2_1; 8.
PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 8.
Transcription regulation; Zinc-finger; Me
RNA-binding; Repeat; Nuclear protein.
DOMAIN

13
276
ZINC_FING
13
37
C2H2-TYPE.
ZN_FING
105
129
C2H2-TYPE.
ZN_FING
105
129
C2H2-TYPE.
ZN_FING
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129
C2H2-TYPE.
ZN_FING
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216
C2H2-TYPE.
ZN_FING
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214
C2H2-TYPE.
ZN_FING
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C2H2-TYPE.
ZN_FING
142
212
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C2H2-TYPE.
ZN_FING
251
246
C2H2-TYPE.
ZN_FING
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276
CH2-TYPE.
ZN_FING
252
ZN_FING
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ZN_FING
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ZH2-TYPE.
ZN_F
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BINDS THE TRANSCRIBED SS RNA'S.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: SYNTHESIZED
LEVELS, IN SOMATIC CELLS.
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S09653; S09653.
P03001; 1TF6.
Similarity
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C2H3-TYPE.
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HSSP; P03001; 1TF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bufo americanus (American toad)
Eukaryota; Metazoa; Chordata; C
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P34694;
                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X58366; CAA41259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparison of the sequence and structure of transcription fact IIIA from Bufo americanus and Rana pipiens.";
Gene 120:197-206(1992).
-!- FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR)
APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III.
BINDS THE TRANSCRIBED 5S RNA'S.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-binding;
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154 CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKG--CSFVAKTWTELLKHVRE
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                                                                      HTGEKPFYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ 153
                                           HTGEKPCKCETENCNLAFTTASNMRLHFKRAHSSPAQVYVCYFADCGQQFRKHNQLKIHQ
                                                                                                                                     PVVYKRFICSFPDCNATYNKNRKLQAHLCKHTGERPFPCTYEGCEKGFVTLHHLNRHVLS
                                                                                                                                                                                                                                    189;
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00028; ZINC_FINGER_C2H2_1; 8.
PS50157; ZINC_FINGER_C2H2_2; 8.
PS50157; ZINC_FINGER_C2H2_2; 8.
ntion regulation; Zinc-finger; Metal-binding; DNA-binding;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular biology of vertebrate transcription factor IIIA: clo
and characterization of TFIIIA from channel catfish oocytes.";
Gene 203:103-112(1997).

-i- FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR)
APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED
CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III.
BINDS THE TRANSCRIPED 5S RNA'S (BY SIMILARITY).
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P79797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA).
                                                                                                                                                                                                   PRINTS; PR00048; ZINCFINGER. SMART; SM00355; ZnF_C2H2; 9.
                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as last scontent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriforme Ictaluridae; Ictalurus.
                                                                                                                                                              Transcription
                                                                                                                                                                        PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
                                                                                                                                                                                                                                InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 9.
                                                                                                                                                                                                                                                                      EMBL; 268499; CAA92808.1;
                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogilvie M.K., Hanas
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                                                                                                                                                RNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90235278; PubMed-2331751;
Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
"A finger protein structurally similar to TFIIIA that binds exclusively to 5s RNA in Xenopus.";
Cell 61:293-300(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                               EMBL; M32473; AAA49714.1; -. PIR; C34895; C34895. HSSP; P03001; ITF3.
                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43_XENLA
SMART; SM00355; Znf_C2H2; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                           Pfam; PF00096; zf-C2H2; 9. PRINTS; PR00048; ZINCFINGER.
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                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: P43 IS A 5S RNA BINDING PROTEIN WHICH IS CONSTITUENT OF OCCYTES AND COMPRISES PART OF A 42S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWO MOLECULES OF P50 (EF1-ALPHA) AND ONE MOLECULE OF THE 5S RNA BINDING PROTEIN 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIBONUCLEOPROTEIN STORAGE PARTICLE.
SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHICH CONTAINS ONE MOLECULE OF 5S RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILCEVCRKTFKRKDYLKQH-MKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVC-QKGCSFVAKTWTELLKHVRETHKEE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPYQCLEDGCSESFISTAGLKNHVERVHQHKEKHYVCDYEGCAKEFRKKKQLRSHKCEHM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDDSELPAQLHGLSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QGQGLSL 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
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                                                                                                                       IPR000822; Znf_C2H2
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Pred. No. 1.1e-55;
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MBL outstation -
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
ZN_FING
                                                                                                                                                                            Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
"A finger protein structurally similar to TFIIIA that binds exclusively to 5S RNA in Xenopus.";
Cell 61:293-300(1990).
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                 MEDLINE=90235278; PubMed=2331751;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID-8354;
                                                                                                                                                                                                                                                                                    Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 101
                                                                                                 RIBONUCLEOPROTEIN STORAGE PARTICLE.
SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF WHICH CONTAINS ONE MOLECULE OF 5S RNA, THREE MOLECULES OF TRNA, TWO MOLECULES OF P50 (EF1-ALPHA) AND ONE MOLECULE OF THE 5S RNA
                                                                                                                                                    FUNCTION: P43 IS A 5S RNA BINDING PROCONSTITUENT OF OOCYTES AND COMPRISES
                                                                                      TWO MOLECULES OF P5
BINDING PROTEIN 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ-KGCSFVAKTWTELLKHVRETHKEEILCE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVCDVPGCSWKSSSVAKLVAHQKRHRGYRCSYEGCQTVSPTWTALQTHVKK-HPLELQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPTAGCKMTFSTKKSLSRHKLYKH-GEAVPLKCFVPGCKRSFRKKRALRRHLSVHSNEPL
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38.1%;
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ZXDB_HUMAN
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Best Local Similarity
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                          P98169: O9UBB3;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2091 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger X-linked protein ZXDB.
        MEDLINE-94093547; PubMed-8268913; Greig G.M., Sharp C.B., Carrel L., Willard H.F.; "Duplicated zinc finger protein genes on the proximal short arm the human X chromosome: isolation, characterization and
                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0048; ZINCFINGER. SMART; SM00355; ZnF_C2H2; 9.
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PIR; A34895; A
X-inactivation studies. ";
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  ZXDB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc-finger;
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                                                     TISSUE=Brain;
                                                                                  Submitted (MAR-1999) to
                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                              SEQUENCE OF 307-709
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                                                                                                                                                                                                                                                                                                          270
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                                                                                                                                                                                                                                                                                                                                                                                           IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ-KGCSFVAKTWTELLKHV
                                                                                                                                                                                                                                                                                                                                                                                                                MKRHLTLKKHSCPTAGCKMTFSTKKSLSRHKLYKH-GDAVPLKCSVPGCKRSFRKKRALR
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                                                                                                                                                                                                                                                                                                                             KK-HPLELQCAACKKPFKKASALRRHKATHAKNPLQLPCPRQDCDKIFSTVFNLTHHLRK
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IPR000822; Znf_C2H2.
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Best Local
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-!- SUBCELLULAR LOCATION: Nuclear (
-!- TISSUE SPECIFICITY: UBIQUITOUS.
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SMART; SM00355; ZnF_C2H2;
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16-OCT-2001 (Rel. 40, La

16-OCT-2001 (Rel. 40, La

16-OCT-2001 (Rel. 40, La
                                                                                                                                                                                                   PRINTS; PRO0048; ZINCFINGER.
ProDom; PD0000003; Znf_C2H2; 7.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 16.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C
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Lamerdin J. E., McGready P.M., Skowronski E., Sakaldasis G.,

Burkhart-Schultz K., Gordon L., Dlas J., Scott D., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,

Brler A., Christensen M., Georgescu A., Avila J., Attix C.,

Andreise T., Trankheim M., Amico-Keller G., Coefield J., Duarte S.,

Incas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
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Submitted
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                             PROSITE; PS50805; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1

Transcription regulation; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00096; zf-C2H2; 16. Pfam; PF01352; KRAB; 1.
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EMBL; M61873; AAA83548.1; -.
PIR; H39384; H39384
HSSP; P08046; 1A1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-191 FROM MEDLINE-91219421; PubMe
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InterPro; IPR000822; Znf_C2H2.
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603975; -.
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Best Local
                                 MEDLINE-9004068; PubMed-2509712;
Nietfeld W., El-Baradi T., Mentzel H.
Poeting A., Knoechel W.;
"Second-order repeats in Xenopus laev
J. Wol. Biol. 208:639-659(1989).
PIR; S06578; S06578.
HSSP, P25490; 1ZNM.
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P18729;
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                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.
                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sanotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
Gastrula zinc finger protein XLCGF57.1 (Fragment).
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                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COK-GCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKOHMKTHAPERDVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCEECGKAFNQSSSLTKH-----KKIHTGEKPYKCEECGKAFNQSSTLIKHKKIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQN-----GESPNCVEDKMLST
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Pro; IPR000822; Zn1
PF00096; Zf-C2H2;
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01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger X-linked protein ZXDA.
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ZN_FING
ZN_FIN
                  MEDLINE-94093547; pubMed-8268913;
Greig G.M., Sharp C.B., Carrel L., Willard H.F.;
"Duplicated zinc finger protein genes on the proximal short
the human X chromosome: isolation, characterization and
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMARR; SM00355; ZnF_C2H2; 12.
PROSITE; PS00028; ZINC_FINGER
PROSITE; PS50157; ZINC_FINGER
Zinc-finger; Metal-binding; D
X-inactivation
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZXDA_HUMAN
                                                                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                  Submitted (JUN-1999) to
                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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0157; ZINC_FINGER_C2H2_2; 12.
Metal-binding; DNA-binding; Repeat.
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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nes 122;
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Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 2:1611-1618(1993).
-!- SUBCELLULAR LOCATION: Nuclear (
-!- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
Zinc-finger; Metal-binding; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 300235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL034396; CAB46717.1; -. EMBL; L14787; AAC37521.1; -. HSSP; P03001; 1TF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:13198; ZXDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000822; Znf_C2H2. Pfam; PF00096; zf-C2H2; 10.
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CPISSCNKLFTSKHSMKTHM----VKRHKVGQDL
                                                              ATGCDOKFNTKSNLKKHF-----------ERKHENQOKQYICSF 136
                                                                                                                                                                                                                                                                                                                              PAVVAESVSSLTIADAFIAAGESSAPTPPRPAL-----PRRFICSFPD------
                       LKV----KKSREKRSLASHLSGYIPPKRKQGQGL
                                                GCGKSFTRAEHLKGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSR
                                                                                                   FDGCGWNFTSMSKLLRH---
                                                                                                                                                 SGCKKTFITVSALFSHNRAHFREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCD
                                                                                                                                                                          EDCKKTFKKHQQLKIHQCQHTNE-PLFKCTQEGCGKHFASPSKLKRHAKAHEG----YVCQ
                                                                                                                                                                                                   AEGCGKSFTTVYNLKAHMKGHEQENSFKCEVCEESFPTQAKLGAHQRSHFEPERPYQCAF
                                                                                                                                                                                                                                                    CGQTFAKKHQLKMHLLTHSSSQGQRPFKCPLGGCGWTFTTSYKLKRHLQSHDKLRPFGCP
                                                                                                                                                                                                                                                                            CSANYSKAWKLDAHLCKHT---GERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCA 103
                                                                                                                                                                                                                                                                                                       PGDCPELRSDLLLAE - - - PAEPAPAPAPQEEAEGLAAALGPRGLLGSGPGVVLYLCPEAL
                                                                                                                         -KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                    Score 409;
Pred. No. 4
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574
                       339
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.4e-24;
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RESULT 13 Z234_HUMAN

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PITTER REPORTED DO DE LE CONTRE CONTR
                                                                                                                                                                                                                                                                                                          PRINTS; PRO0048; ZINCFINGER.
PRODOM; PRO00003; ZNf_C2H2; 5.
SMART; SM00349; KRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00345; ZNF_C2H2; 19.
PROSITE: PS50805; KRAB; 1.
PROSITE: PS50805; KRAB; 1.
PROSITE: PS50805; KRAB; 1.
PROSITE: PS50157; ZINC_FINGER_C2H2_1; 18.
PROSITE: PS50157; ZINC_FINGER_C2H2_2; 19.
Transcription reg
Nuclear protein;
DOMAIN
DOMAIN
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DOMAIN
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ZN_FING
ZN_FIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene cluster.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databas
-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
-!- SUBGELJULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abrink M., Aveskogh M., Hellman L.;
*Isolation of cDNA clones for 42 different Kruppel-related proteins expressed in the human monoblast cell line U-937.*
DNA Cell Biol. 14:125-136(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00096; zf-C2H2; 19.
Pfam; PF01352; KRAB; 1.
PRINTS: pp00000
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ZNF234 OR ZNF269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF228417; AAF34785.1; -.
EMBL; X78927; CAA55527.1; -.
EMBL; AC074431; AAF88104.1; -.
HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kodoyianni V., Ge Y., Severin J., Krummel G.K., Grable L., Kvikstad E., Gordon L., Shannon M., Brower A., Olsen A.S., Wylkstad E. analysis of a 1Mb region in 19q13.2 containing a gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 7-698 FROM N.A.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Differential expansion of homologous zinc-finger gene families human chromosome 19q13.2 and mouse chromosome 7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shannon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-73 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z234_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:13027; ZNF234.
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       KRAB.

KRNB.

ZINC FINGE:

C2H2-TYPE.

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C2H2-TYPE.
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                                                                                                                                                                                   FINGERS
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19
                                                                                                                                                                                                                                                                                                                     Zinc-finger; Metal-binding;
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RESULT 14
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ZN41_HUMAN STANDAKU;
P51814; Q9UMC4; Q96LE8; Q9UMV5; Q9UMV6; Q9UMW0;
Q9UMW0; Q9UWN1;
Q1-CCT_1996 (Rel. 34, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                             Rosati M., Franze A., Matarazzo M.R., Grimaldi G.; "Coding region intron/exon organization, alternative splicing and x-chromosome inactivation of the KRAB/FPB-domain-containing human finger gene ZNF41."; Cytogenet. Cell Genet. 85:291-296(1999).
                                                                                                                                                                                      SEQUENCE FROM N.A.,
MEDLINE-99380103; PI
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                   MEDLINE=91244317;
                                       SEQUENCE OF 280-821 FROM N.
                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKSFRMKIHYQVHLVVHTGEKPYKCEVCGKAFRQSSYLKIHLKAHSVQKPF-KC--EECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCDOKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKTWTELLKH----VRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEGCGKHFASPSKLKRHAKAHEG---YVCQ---KG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGFNQSSRLQIHQL-IHTGEKPYKCEECGKGFNRRADLKIHCRIHTGEKPYNCEECGKVF
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                   PubMed-2037297;
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N., Rocchi M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 406; DB Pred. No. 6.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            936D390D02E6746B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UMV6; Q9UMV7; Q9UMV8; Q9UMV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                              SPLICING
Marino
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Grimaldi
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Nuclear protein; F
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SMART; SM00355; ZnF_CZHI; 17.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 17.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown A.;
Submitted (AUG-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 142-821 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000822; Zni
Pfam; PF00096; Zf-C2H2;
Pfam; PF01352; KRAB; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and expression analysis of a human zinc finger gene (ZNF41) located on the short arm of the X chromosome."; Genomics 9:728-736(1991).
                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001909; KRAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FINGER PROTEINS.
SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: At least 8 isoforms; 1 (shown here), 2, 4, 5, 6, 7 and 8; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (AUG-2001) to the EMBL/GenBank/DDBJ dat FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X60155; CAB51740.1;

AJ010018; CAB53035.1;

AJ010018; CAB53037.1;

AJ010019; CAB53037.1;

AJ010020; CAB53038.1;

AJ010021; CAB53038.1;

AJ010021; CAB53039.1;

AJ010022; CAB53040.1;

AJ010023; CAB53041.1;

AJ010023; CAB53041.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Znf_C2H2;
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H2; 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                                                   C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                        C2H2-TYPE.
C2H2-TYPE
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C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                 C2H2-TYPE.
                                    PDLSPGPKGRSSADHAALN -> MGTLPHGPRPWLQRDVAA
HV (IN ISOFORM 7 AND ISOFORM 2).
                     MAANGDSPPWSPALAAEGRGSSCEVRRERTPEARIHSVKRY
                                                                              MAANGDSPPWSPALAAEGRGSSCEVRRERTPEARIHSVKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEGENERATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions
MGTLPHGPRPWLQRDVAAHV
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YE73_HUMAN
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Best Local S
Matches 106
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SEQUENCE
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Q9P255;
         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          Hypothetical zinc KIAA1473.
                                                                                                                                                                                                           Nagase T., Kikuno R., Ishikawa K.-I., "Prediction of the coding sequences of The complete sequences of 100 new cDN.
                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=20277482; PubMed=10819331;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                    IIs-JUN-2002 (Rel. 41, Created)
IIs-JUN-2002 (Rel. 41, Last sequence update)
IIs-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical zinc finger protein KIAA1473 (Fragment).
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                          FUNCTION: MAY FUNCTION AS A SUBCELLULAR LOCATION: Nucle SIMILARITY: BELONGS TO THE
                                                                                                          FINGER PROTEINS.
SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                  large proteins in vitro."; Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TECOKAFTORSNLIKHOKMHSGEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKVKKSREKRS-LASHLSGYIPPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAE---CGKAFTDQSNLIKH---QKTHTGEXPYKCN---GCGKAFIWKSRLKIHQKSHIGERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CS--DCGKSFTKKSQLHVHQRIHTGEKPYIC--TECGKVFTHRTNLTTHQKTHTGEKPYM 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 10:
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Pred. No. 1.1e-23;
6; Mismatches 121
                                                                                                                                          A TRANSCRIPTION lear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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(IN ISOFORM 7 AND ISOFORM
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Search completed: February 10, 2003, 17:45:49 Job time : 26 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 20.1%; Score 403; DB 1; Length 574; Best Local Similarity 31.0%; Pred. No. 8.9e-24; Matches 106; Conservative 47; Mismatches 121; Indels
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Probomo3; Znf_C2H2; 2.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 13.
SMART; SM00355; ZnF_C2H2; 13.
PROSITE; PS0002B; KRAB; 1.
PROSITE; PS0002B; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS0002B; ZINC_FINGER_C2H2_2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
Zinc-finger;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 ECGKAYNETSNLSTHKRIHTGKKPYKC--EECGKAFNRLSHLTTHKIIHTGKKPYKCEE- 272
                                                                                                                                                                                                                            312 VKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESP-NCVE 352
                                                                                                                                                                                                                                                                                                                                                                             255 RTYTTVFNLQSHILS---FHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                 YEECGKAFNQSSHLTTH-----KMIHTGEKPYKCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKAFKQSSTLTTHKRIHAGEKFYKCEVCSKAFSRFSHLTTHKRIHTGEKPY-KC--EECG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFVAKTWTELLKHVRETHKEEIL-CEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGKAFSQSSTLTTHKIIHTGEKFYKC · · EECGKAFSQLSHLTTHKRIHSGEKPYKCEE · C 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CGKAFNQSANLTTH-KRIHTGEKPYKCEECGRAFSQSSTLTAHKIIHAGEKPYKC--EE 328
                                                                                                                                                                                                                                                                                                          K----AFNLSSQLTTHKIIHTGEKPYKCEE--CGKAFNQSSTLSKHKVIHTGEK---PYK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Transcription regulation; DNA-binding;
Metal-binding; Nuclear protein; Repeat.
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C2H2-TYPE.
C2H2-TYPE (DEGENERATE).
C2H2-TYPE.
C2H3-TYPE.
W; 482E5F1176ECA5B0 CRC64;
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C2H2-TYPE.
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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    No. is the number of results predicted by chance to have a
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1: /cgn2_6/ptodata/1,
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4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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US-08-570-227A-1

US-09-077-991-1

US-09-657-042A-3

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US-08-523-376-2
Query Match
Best Local Similarity
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ALIGNMENTS

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20..1288
; IDENTIFICATION METHOD:
US-08-523-376-2
                                                                                                                                                                                                                                            FILING DALL.

CLASSIFICATION: 536

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08523376 Patent No. 5808030 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, M
STREET: 2100 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2100 Pennsylvani
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA
CLONE: OTK7
                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sadahito, SIN
TITLE OF INVENTION: hTFIIIA GENE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/523,376
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linear
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Kouichi, OZAKI
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Satoshi, TAKEDA
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Score 1170; DB 1;
Pred. No. 2.1e-303;
               Length 1399;
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5808030 GENERAL INFORMATION:
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                         Matches 1203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTED:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Mac STREET: 2100 Pennsylvania Avenue, N CITY: Washington STATE: D.C.
COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSUTOMU, FUJIWARA
APPLICANT: SATOSHI, TAKEDA
APPLICANT: YOSHIKAZU, SHIMADA
APPLICANT: KOUİCHI, OZAKI
APPLICANT: SAĞAHİCO, SIN
TITLE OF INVENTION: hTFIIIA GENE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1269 base pair
TYPE: nucleic acid
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                                                                  AGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCGCGCCCGCGCGTTCCCAGGAGGTTCATCTG
                              TCCGCCGGCCGTGGTCGCCGAGTCGGTGTCGTCCTTGACCATCGCCGACGCGTTCATTGC
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Pred. No. 1.3e
0; Mismatches
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                                                                                                 TCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAC-GGAGTTTGG
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GENERAL INFORMATION:

APPLICANT: Song, An M.

APPLICANT: Chen, Ya-Fen

APPLICANT: Chen, Ya-Fen

APPLICANT: Chen, Ya-Fen

TITLE OF INVENTION: REFLAT-1: A Transcription Factor Tha

TITLE OF INVENTION: Activates RANTES Gene Expression

FILE REFERENCE: SUN-113p

CURRENT APPLICATION NUMBER: US/09/492,985

CURRENT FILING DAYE: 2000-01-27

EARLIER APPLICATION NUMBER: 60/117,576

EARLIER APPLICATION NUMBER: 50/117,576

EARLIER FILING DAYE: 1999-01-27

NUMBER OF SEQ ID NOS: 11
                                                                                                          APPLICANT: Song, An M.
APPLICANT: Chen, Ya-Fen
APPLICANT: Krensky, Alan M.
APPLICANT: Krensky, Alan M.
TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
TITLE OF INVENTION: Activates RANTES Gene Expression
FILE REFERENCE: SUN-113P
CURRENT APPLICATION UNMEER: US/09/492,985
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,576
EARLIER APPLICATION NUMBER: 60/117,576
INUMBER OF SEO ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: mouse
US-09-492-985-11
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Best Local
                                                                           LENGTH: 14
TYPE: DNA
                          ORGANISM: homo sapien FEATURE:
OTHER INFORMATION: synthetic oligonucleotide probe
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Pred. No. 2e-07;
0; Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cooke, Michael Paul
APPLICANT: Holness, Claire
APPLICANT: Sirenko, Oksana
TITLE OF INVENTION: NO. 6451558el Genes in th
FILE REFERENCE: 4-30629A/SYS
CURRENT APPLICATION NUMBER: US/09/362,123A
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 09/128,310
PRIOR FILING DATE: 1998-08-03
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US-09-362-123A-3
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Best Local Similarity
Matches 142; Conserv
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SOFTWARE: PatentIn V
SEQ ID NO 3
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                 FEATURE:
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    1323
                                                                           1263 TGCCTTCAGCCAGGGCTCCTCGCTCTTTAAGCACCAGGGGTGCACACAGGCGAGAAGCC 1322
                                                                                                 178 TGCAGCCGGCGAGAGCTCCGACCCCGCCGCGCCCCCGCGCTTCCCAGGAGGTTCAT 237
                        238 CTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 AGTCGCGCCGACCTCGAGTCCCCGCAGAGGAAGCACAAGTGCCACTACGCGGGCTGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCCCCCAGCCCGGCGTGGAGCCGAGCCCGAGGCGGGGGCTGGAGCCCGAGCGG
CTTCGCCTGCCCACAGTGCGGCCGCGCCCTTTAGCCACAGCTCCAACCTCACCCAGCACCA 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTTCGCCTGCAGCTGGCAGGACTGCAACAAGAAGTTCGCGCGCTCCGACGAGCTGGCG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTACCATCTGAGC
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                                                                                                                                                          Conservative
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54.6%;
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48.9%;
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                                                                                                                                                      Score 58.8; DB 4;
Pred. No. 4.1e-06;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61.4; DB Pred. No. 6e-07;
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                                                                                                                                                                                           Length 2992;
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Zic 1 Protein gene; Genbank Acession D76435
US-09-234-332-5
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                                                                                                                                                                                                                                                                               RESULT 7
US-08-570-227A-1
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LENGTH: 3138
TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                         Sequence 1, Application US/08570227A Patent No. 5981217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.5%;
Best Local Similarity 55.2%;
Matches 107; Conservative
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APPLICANT: Michel F. Levesque, M.D.
APPLICANT: TOomas Neuman, Ph.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILE REFERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
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                                                                             APPLICANT: Subramaniam, M.
APPLICANT: Speisberg, T. C.
TITLE OF INVENTION: DAS ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE I
TITLE OF INVENTION: BY OSTEOBLASTS
                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1497 GTGTACGCAGTGTGGCCGCG 1516
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  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGTGGCAAGGTCTTCGCGCGCGCTCCGAGAATTTAAAGATCCACAAAAAGGACGCACACA 1761
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  P.O.
Schwegman,
O. Box 2938
                   Lundberg,
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Pred. No. 5e-05;
0; Mismatches
                     Woessner &
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COMPUTER READABLE FORM:

55402

MEDIUM TYPE: Diskette

COUNTRY:

Minneapolis
MN
Y: USA

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APPLICANT: Subtamaniam, M.
APPLICANT: Spelsberg, T.C.
APPLICANT: Spelsberg, T.C.
APPLICANT: Roche, P.C.
TITLE OF INVENTION: TGF-Beta inducible early fac
TITLE OF INVENTION: TGF-Beta inducible early fac
TITLE OF INVENTION: TGF-Beta inducible early fac
TITLE OF INVENTION: TGF-Beta inducible early fac
TITLE OF INVENTION: TGF-Beta inducible early fac
TITLE OF INVENTION: TGF-Beta inducible early fac
TELE REFERENCE: 150.157029
CURRENT APPLICATION NUMBER: US/09/077,991
CURRENT FILING DATE: 1996-12-11
EARLIER APPLICATION NUMBER: US 08/570,227
EARLIER APPLICATION NUMBER: US 08/570,227
EARLIER FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 54.6%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09077991 Patent No. 6207375
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APPLICATION NUMBER: US/G
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2881 base pairs
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.157US1
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SOFTWARE: FastSEQ Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 612-359-3263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAATTTGCGTG 1378
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Pred. No. 0.00013;
0; Mismatches 88;
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                                                                                                                                                                                                                   detect breast cancer
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; ORGANISM: Homo sapiens
US-09-077-991-1
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Best Local Similarity 54.6%;
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                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEITLINGER,
APPLICANT: FALKNER, F.
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TOPOLOGY: line
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 1
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TTD: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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CITY: Alexandria
                                                      LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                              (703)683-4109
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Pred. No. 0.00013;
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; LOCATION: (79)...(3399)
US-09-657-042A-3
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US-08-232-463-14
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US-09-657-042A-3
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SEQ ID NO 3
LENGTH: 3600
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 149; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: RTS-0148
CURRENT APPLICATION NUMBER: US/09/657,042A
CURRENT FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: C. Frank Ber APPLICANT: Jacqueline Wyatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                          1057
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                                                                                                                                                         937 ATGCTGGTGGTTCACATGCGCAGACACACTGGCGAGAAGCCACACAAGTGCACGTTTGAA 996
                                                                                                                                                                                      811 TAAGCAACACATGAAAACTCATGCCCCAGAAAGGGA 846
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                                            GGAGAAAAGCCGTTTGTTTGTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCA 460
                                                                                         GGGTGCCGGAAGTCATACTCACGCCTCGAAAACCTGAAGACGCACCTGCGGTCACACACG
                                                                                                                         GGGTGTGGCAAGGCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACA 400
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                       GGTGAGAAGCCATACATGTGTGAGCACGAGGGCTGCAGTAAAGCCCTTCAGCAATGCCAGT 1116
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                                                                                                                                                                                                                           Score 52.6; DB 4; Length 3600; Pred. No. 0.0002; O; Mismatches 139; Indels 3
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US-08-946-241B-1
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US-09-907-843-3
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SEQ ID NO 3
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSIO FILE REFERENCE: RTS-0279
CURRENT APPLICATION UNMEER: US/09/907,843
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                             Sequence 1, Application US/08946241B Patent No. 5928941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                ADDRESSEE: Fish & RICHARDS STREET: 225 Franklin Street
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es 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 TTTGAAGACTGTAAGAAGA 539
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   Diskette
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                                                                                                                                                                           REPRESSOR KRUPPEL-LIKE FACTOR
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Pred. No. 0.00063;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA.Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/946,241B FILING DATE: 07-OCT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/030,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
TYPE: nucleic acid
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FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,241B
FILING DATE: 07-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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TELSFAX: 200154
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                                                                                       COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                STREET: 225 |
CITY: Boston
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APPLICATION NUMBER:
                                                                                                                                                                                              COUNTRY:
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                                                                                    FastSEQ Version 2.0
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60/030,035
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Best Local Similarity 55.0%;
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APPLICANT: Lee, Mu-En
APPLICANT: McA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR
                         APPLICATION NUMBER: US/09/309,05
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/946,241
FILING DATE: 07-OCT-1997
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 107-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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LENGTH: 1889 base pairs
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FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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REGISTRATION NUMBER:
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EDNESS: single
                 Creason,
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US-09-309-053-1
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TELEX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/946,241
FILING DATE: 07-OCT-1997
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICANT: McA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
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                                                          REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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                TELEFAX: 01.
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                                                        TELEPHONE:
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                                                                                                                               NAME: Creason, Gary L.
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225 Franklin Street
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US-09-309-053-8
Search completed: February 10, 2003, 12:48:08 Job time: 109.257 secs
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Best Local Similarity 55.0%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1889 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                     1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCCGTT 1773
                                                                                                                                                                      1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
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                                                                                                                             355 CTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 414
                                                                                                                                                                                                              295 CCTGTGCAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding Sequence
                                                                                                                                                                                                                                                                                                                                         Score 50.4; DB 3; Length 1
Pred. No. 0.00059;
0; Mismatches 81; Indels
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Maximum
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Perfect score:
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Maximum Match
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Gapop 10.0 , Gapext 1.0
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1213
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   Published_Applications_NA: *
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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  10 US-09-920-300A-326
11 US-10-033-528-326
10 US-09-920-300A-689
11 US-10-033-528-689
12 US-09-796-920-4064
10 US-09-920-300A-610
11 US-10-033-528-610
12 US-10-033-528-610
13 US-09-920-300A-610
14 US-09-935-973-2
15 US-09-935-973-1
16 US-09-935-973-1
17 US-09-935-973-1
18 US-09-935-973-1
19 US-09-933-348-5
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13 US-09-933-348-1
14 US-09-933-348-1
15 US-09-933-329-1
16 US-09-933-329-1
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18 US-09-934-329-1
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Sequence 689, App
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Sequence 610, App
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54.6	54.6	54.8	55.4	55.4	55.4	55.4			58.2	58.2	60	60	60.2	60.2	60.6	60.6	60.6	61.8	61.8		63		63	64.6	64.6
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Sequence 119, App	Sequence 119, App	Sequence 1716, Ap	Sequence 137, App	Sequence 73, Appl	Sequence 120, App	Sequence 1613, Ap	35	17	Sequence 4, Appli	16, A	642, /	4925,	Sequence 417, App	211,	Sequence 28, Appl	Sequence 17, Appl	29, A	Sequence 1647, Ap		76,	Sequence 10, Appl	Sequence 2, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl

ALIGNMENTS

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; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for W
; SEQ ID NO 326
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-326
                                                                                                                                                                                                                                                                                                                            Query Match 34.5%;
Best Local Similarity 99.8%;
Matches 419; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/920,300A CURRENT FILING DATE: 2001-07-31 NUMBER OF SEQ ID NOS: 1789 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                             CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTTAATCTCCAAAGCCAT 913
                                                                               ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                         Score 418.4; DB 10;
Pred. No. 1.4e-103;
Pred. No. 1.4e-113;
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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 326
SEQ ID NO 326
SEQ ID NO 326
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-326
US-09-20-300A-689
; Sequence 689, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
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Matches 419; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 326, Application US/10033528 Patent No. US20020131971A1
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Pred. No. 1.4e-103;
O; Mismatches 1;
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                               US-10-033-528-689
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Best Local Similarity 99.5%;
Matches 418; Conservative
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 Query Match
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APPLICANT: Meagher, Madeleine Joy
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 689
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCE FILE REFERENCE: 210121, 547C1 (CURRENT APPLICATION NUMBER: US/10/033,528) CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTMARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 689
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 689, Application US/10033528 Patent No. US20020131971A1
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
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Pred. No. 3.7e-103;
0; Mismatches 2;
Score 416.8;
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PRIOR FILING DATE: 2000-0218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR PILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                      CURRENT FILLING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILLING DATE: 2000-03-01
PRIOR PRIOR APPLICATION NUMBER: 60/200,545
PRIOR EILLING DATE: 2000-04-27
PRIOR PRILING DATE: 2000-04-27
PRIOR FILLING DATE: 2000-04-27
PRIOR FILLING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/2020,099
PRIOR FILLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/2020,094
PRIOR APPLICATION NUMBER: 60/2020,094
PRIOR FILLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/2020,094
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                                         PRIOR APPLICATION NO......PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
WINDER OF SEQ ID NOS: 9597
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jaul A.
APPLICANT: Mannion, Compositions and methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077.001200
                    NUMBER OF SEQ ID I
SOFTWARE: FastSEQ
SEQ ID NO 4064
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RESULT 7
US-10-033-528-610
; Sequence 610, Application US/10033528
; Patent No. US20020131971A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.3%; Score 234; DB 10; Best Local Similarity 100.0%; Pred. No. 7.1e-54; Matches 234; Conservative 0; Mismatches 0;
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LENGTH: 234
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Best Local :
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APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
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CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547C1

CURRENT APPLICATION NUMBER: US/10/033,528

CURRENT FILING DATE: 2001-12-26

NUMBER OF SEQ ID NOS: 1896

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 610

LENGTH: 234
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BUTMER, Glenna C.
APPLICANT: Brown, Joseph P.
APPLICANT: LifeSpan BloSciences, Inc.
APPLICANT: LifeSpan BloSciences, Inc.
TITLE OF INVENTION: Nucleic Acid Sequences a
TITLE OF INVENTION: Associated With Aging
FILE REFERENCE: 017473-00111005
CURRENT APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1999-04-14
FEARLIER APPLICATION UMMBER: US 60/081,887
EARLIER APPLICATION UMMBER: US 60/081,887
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 362
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US-09-292-758-68
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Best Local Similarity
Matches 263; Conserv
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Best Local 9
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APPLICANT: Meagher, Madeleine Joy
                  1003 GCATGCTGTTGTACATGATCCTGACAAGAAGAAATGAAGCTC-AAAGTCAAAAAATCTC 1061
                                                                        362 TGTGTGAACATGCTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTTAG 303
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                                                                                                  946 TGTGTGTGAACATGCTGGCTGTGGCAAAA--CATTTGCAATGAAACAAAGTCTCAC-TAG 1002
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GCATGCTGTTGTACATGATCCTGACAAGAAGAAAATGAAGCTCAAAAGTCAAAAATCTC
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Pred. No. 7.1e-54;
0; Mismatches 0;
                                                                                                                                                        Score 226; DB 9;
Pred. No. 1.3e-51;
0; Mismatches 5
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Sequence 2, Application US/09995973
Publication No. US20030024006A1
GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: CHOO, Yen
TITLE OF INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/09/995,973
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 947
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US-09-995-973-2
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                         CAACACAAAATCAAACTTGAAGAAACATTTTGAACGCAAACATGAAAAATCAACAAAAAACA 507
                                                                                                                                                                                                                                                                                          TCTGACTCACACAGGAGAAAAGCCGTTTGTTGTGCAGCCACTGGCTGTGATCAAAAATT 447
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                 ACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 681
                                                                                                                                    ATATATATGCAGTTTTGAAGAACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAAT 567
                                                                                                                                                                                                      TACTACAAAGGCAAACATGAAGAAGCACTTTAACAGATTCCATAACATCAAGATCTGCGT 325
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                                                                  TCATCAGTTCAGTCACACACAGCAGCTGCCGTATGCCTTGCCCTGTCGAGTCCTGCGATCG
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57.6%;
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Pred. No. 1.9e-31;
0; Mismatches 201;
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RESULT 10 US-09-732-348-5

Indels Length

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995; 0

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Sequence 1, Application US/09995973
Publication No. US20030024006A1
GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: CHOO, Yen
TITLE OF INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/09/995,973
CURRENT FILING DATE: 2002-03-19
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US-09-995-973-1
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SEQ ID NO 5
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APPLICANT: Yen Choo, et al.
APPLICANT: Yen Choo, et al.
TITLE OF INVENTION: Regulated Gene Expression
FILE REFERENCE: 674538-2001
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 21
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LOCATION: (909)..(938)
OTHER INFORMATION: c-myc tag, other features except transactivation
OTHER INFORMATION: ted above) same as SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (723)..(908)
OTHER INFORMATION: transactivation domain
OTHER INFORMATION: listed below) same as $
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TYPE: DNA
ORGANISM: Artificial Sequence
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Local Similarity 57.6%;
es 273; Conservating
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                                                                                                                                                                                                                                 CCGCTTTTCTCGCTCGGATGAGCTTACCCGCCATATCCGCATCCACACACGCCA 499
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Pred. No. 1.9e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 947;
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    OTHER INFORMATION: TFIIIA/Zif-vP16
US-09-995-973-1
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US-09-732-348-4
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                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 995
                           NAME/KEY: misc_feature
LOCATION: (15)..(17)
OTHER INFORMATION: translational ir
NAME/KEY: misc_feature
LOCATION: (16)..(416)
OTHER INFORMATION: Fingers 1 to 4 c
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Best Local
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                                                                                                                                                                                                                                                                                                APPLICANT: Yen Choo, et al.
TITLE OF INVENTION: Regulated Gene Expression
FILE REFERENCE: 674538-2001
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                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
NAME/KEY: misc_feature LOCATION: (308)..(416)
                                                                                                                                           FEATURE:
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Pred. No. 1.9
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NAME/KEY: misc_feature
LOCATION: (701)...(722)
OTHER INFORMATION: Nuclear Loc
NAME/KEY: misc_feature
LOCATION: (957)...(986)
OTHER INFORMATION: c-myc tag
US-09-732-348-4
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                              PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5443
LENGTH: 449
                                                                                                                                                                                                                                                                                             Sequence 5443, Application Patent No. US20020110850A1 GENERAL INFORMATION:
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Best Local Similarity 57.6%;
Matches 273; Conservative
                                                                                                                                                                                 APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILLING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                 APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William
APPLICANT: L1, Haodong
APPLICANT: Rosen, Craig A.
                 LENGTH: 44
TYPE: DNA
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LOCATION: (417)..(689)
OTHER INFORMATION: three fingers
ORGANISM: Homo sapiens
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Pred. No. 1.9e-31;
0; Mismatches 201;
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Best Local Similarity
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OTHER INFORMATION: n equals a.t.g, NAME/KEY: misc feature LOCATION: (448)
OTHER INFORMATION: n equals a.t.g,
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                          418 TTGTGCAGCCACTGGC-TGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATT 476
                                                                                                                                                                                                        TNCNTTGTGGGCAAAAACTGGGACGGGACTTCTGNAACTGTGAGNGAAACCCTTAAGGGG
             TCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAG
                                                                                                                                                      -GAAGACCTTTAAGAAA-----CATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAA 588
                                                                                                                                                                                                                                                            TTGNGCAGCCAATGGCTTGANATCAAAATTCAACACAAAATCAAACTTGAAGAAACATT
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US-09-833-381-1175

ISEQUENCE 1175, Application US/09833381

FACTOR APPLICATION: No. US20020132090A1el Nucleic Acid and Protein Homologs

FILE REFERENCE: S800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NO: 175

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 1111

TYPE: ON:
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-920-300A-1747/c
Sequence 1747, Application US/09920300A
Patent No. US20020136728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1111)
; OTHER INFORMATION: n = A,T,C or
US-09-833-381-1175
; FEATURE:

NAME/KEY: misc_feature
LOCATION: 223, 323
OTHER INFORMATION: n -
US-09-920-300A-1747
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/920,300A CURRENT FILING DATE: 2001-07-31 NUMBER OF SEQ ID NOS: 1789 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1747 LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.1%;
Best Local Similarity 61.1%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangohun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.547
                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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SUMMARIES

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ALIGNMENTS

RESULT 1 HUMIIIA	
LOCUS	HUMIIIA 1381 bp mRNA linear PRI 07-FEB-1999
DEFINITION	nscription
	complete cds.
ACCESSION	D32257
VERSION	D32257.1 GI:1000446
KEYWORDS	GTF3A; Xenopus transcription factor IIIA homologue.
SOURCE	Homo sapiens cDNA to mRNA, clone_lib:librarry of T.Fujiwara, S.Shin
	and Y.Nakamura clone:39H11.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1381)
AUTHORS	Arakawa, H., Nagase, H., Hayashi, N., Ogawa, M., Nagata, M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUL-1994) Yusuke Nakamura, Cancer Institute, Department of Blochemistry; 1-37-1 Kami-Tkebukuro, Toshima-ku, Tokyo 170, Japan (E-mail:nakamura@ganvxl.jfcr.or.jp, Tel:03-9918-0111(ex.4501), Fax:03-3918-0342)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiwara, T., Takahashi, E., Shin, S. and Nakamura, Y. Molecular cloning, characterization, and chromosomal mapping novel human gene (GTF3A) that is highly homologous to Xenopus transcription factor IIIA (3-4), 235-238 (1995)
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CEVGRYTFKRKDYLKQHKTHAPERDVCRCPREGGGTTYTTVFNLQSHILSFHEESRP

FVGEHAGGGKTFAMKQSLTRHAVYHDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRK

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/product="Xenopus transcription factor
/protein_id="BAA06988.1"
/db_xref="GI:1616942"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc
1 (bases 1 to 139)
5 Fujiwara-T., Takeda,S., Shimada,Y., Ozaki,K. and Shin,7
HUMAN TRANSCRIPTIONAL FACTOR IIIA GENE
Patent: JP 1996070870-A 1 19-MAR-1996;
OTSUKA PHARMACEUT CO LTD
OS Homo Sapiens (human)
PN JP 1996070870-A/1
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BASE COUNT
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TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
                                                                       CAAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAAGGGTGTGGCAAGGCCTTCAT
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                                    CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
                                                                                                                                                           TGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAACATTTTTGA
                                                                                                                                                  TGCAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
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FUJIWARA TSUTOMU, TAKEDA SEI, SHIMADA YOS
SHIN TEIKIN
C12N15/09//A61K31/70,A61K48/00,C07H21/04;
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/db_xref="taxon:9606"
1 349 c 354 g 29
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99.3%;
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20. .1288
/product='hTFIIIA p
1289. .1399.
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Pred. No. 1.1e
0; Mismatches
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95347600
                                                                                                             Submitted (25-JAN-1995) Kevin G. Becker, Diseases and Stroke/NIH, Neuroimmunology Pike, Bethesda, MD 20892, USA
                                                                                                                                                                                                        Drew, P.D., Nagle, J.W.,
Becker, K.G.
Cloning and expression
Xenopus TFIIIA
                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                             Direct Submission
                                                                                                                                                       Becker, K.G.
                                                                                                                                                                                                                                             (sites)
                                                                                                                                                                 (bases
                                                                                                                                                                                               159 (2),
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       /sex="female"
/tissue_type="brain; hippocampus"
/clone_lib="Stratagene #936205"
/dev_stage="2 years old"
<1. 1092
                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C2H2-34.10"
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                                                                                                    Location/Qualifiers
note="similar to"
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Primates;
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Xenopus
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TFIIIA encoded
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Branch,
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ch, 9000
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BASE CO
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Best Local Similarity
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AAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT
                                                     AAGCACACGGGGAGAGACCATTTGTTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATC
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/note="encodes:
565. .631
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/product="DNA/RNA-binding protein"
/protein_id="AAA/75623.1"
/protein_id="AAA/75623.1"
/db_xref="G1-644871"
/db_xref="G1-644871"
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829. .895
/note="encodes zinc-finger"
283 c 265 g 262 t
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                                                                                       Direct Submission
Submitted (29-AUG-1994) Kevin G. Becker, National Institute
Neurological Diseases and Stroke/NIH, Neuroimmunology Branch
Rockville Pike, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                      2 (bases 1 to 1098)
Becker, K.G.
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 1098)
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                                                                                                                                                                                                                 Drew, P.D., Nagle, J
                                                                                                                                                                                                                                                                            human
                                                                                                                                                                               Unpublished
                                                                                                                                                                                                      Becker, K.G
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/tissue_type="brain"
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Number 936205"
                                                /organism="Homo sapiens"
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/note="encodes zinc-finger"
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/note="TFIIIA; similar to Xenopus transcription
/IIIA, Swiss-Prot Accession Number P03001"
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/protein_id="AAA21873.1"
/db_xref="GI:551535"
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ISHIDASHI, T., KANEHORI, K., YOSIDA, M., WATANADE, S., ISHIDA, S., ONO, Y., HOTUTA, T., HITAOKA, S., MUTAKAWA, K., TAKİGUCHİ, S., KUSANO, J., WATANADE, M., FUJİMORI, K., TANAİ, H., ISHİDA, M., Yamashita, H., Chiba, Y., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, Morinaga, M., Kawamura, M., Sugiyama, T., Irle, R., Otsuki, T., Sato, Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Suqano, S. AK057993.1 GI:16553988 oligo capping; fis (full insert sequence). Homo sapiens stomach mucosa cDNA to mRNA, clone_lib:STM clone:STM05057. AK057993 1920 bp mRN Homo sapiens cDNA FLJ25264 fis, clone TRANSCRIPTION FACTOR IIIA. Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA linear one STM05057, hi ar PRI 31-OCT-2001 highly similar to

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                 TCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTTAATCTCCAAAGCCA
                                                                                                                                      TAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGAAAGGGATGTATG
                                                                                                                                                                                            GAAACATGTGAGAGAAACCCATAGAGAGGAAATACTATGTGAAGTATGCCGGAAAACATT
                                                                                                                                                                                                             GAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATT
                                                                                                                                                                                                                                                                               CGAGGGCTATGTATGTCAAAAAAGGATGTTCCTTTTGTGGCAAAAACATGGACGGAACTTCT
                                                                                                                                                                                                                                                                                                                                  GGGAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCA
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                                                  TCGCTGTCCAAGAGAAGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCA
                                                                                                                                                                                                                                                               CGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                    TCAGCAGCTGAAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATTCAAGTGTACCCA
AAATCAACAAAAACAATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACA
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Sugano, S. and Suzukl, Y.
Direct Submission
Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Huma
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/db_xreff"taxon:9606"
/clone="STM05057"
/tissue_type="stomach mucosa"
/clone_lib="STM"
/note="cloning vector: pME18SFL
a 462 c 438 g 500 t
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                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-JUN-2001) Biochemistry/Molecular Biology, University of Oklahoma Health Science Center, 800 Research Parkway, Suite 448, Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1298)
Hanas,J.S., Hocker,J.R., Cheng,Y.G., Lerner,M.R., Brackett,D.J.
Hanas,J.S., Hocker,J.R., Madhusudhan,K.T. and Moreland,R.J.
Lightfoot,S.A., Hanas,R.J., Madhusudhan,K.T. and Moreland,R.J.
CDNA cloning, DNA binding, and evolution of mammalian transcri
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AF391799.1 GI:18448381
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Hanas, J.S., Hocker, J
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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  PAALLTVC"
a 368 c
                                    /product="transcription factor IIIA"
/protein_id="AAL69686.1"
/protein_id="AAL69686.1"
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/db_xref="GI:18448382"
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NPQKQYLCSYEGCKKAFKKHQOLTHITGEKPFVCTHEGCGKHFASPSKRHKRHGK
VHEGYLCQKGCSFMGKTWTELLKHMREAHKEDITCNVCQRMFTKRDYLKQHMKTHAPE
RDVYRCPRQGCGRTYTTVFNLOSHILSFHEEKRPFVCHAGCGKTFAMKQSLMRHSVV
HDPDKKRMKLKVRAPRERRSLASRLSGYFPPKRKQEPDYSLPNASAESSSSPEAQLPP
                                                                                                                                                                                                                                                                  /note="TFIIIA; Cys2His2 zinc
Xenopus laevis transcription
Accession Number P03001"
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                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                  CGGAGTTTGGCCTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGC
                                                                                                 GTTGTACATGATCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAAAATCTCGTGAAAAA
                                                                                                                                             TGTGAACATGCTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCT
                                                                                                                                                                                 ACCGTGTTCAACCTGCAGAGCCACATTCTCCTCCTTCCACGAGGAAAAGCGCCCATTTGTG
                                                                                                                                                                                                                                             CATGCCCCAGAAAGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACT
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                                                                                                                                  TGTGAGCACGCTGGGCTGTGGCAAGACATTCGCAATGAAACAGAGTCTCATGAGGCACAGT
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Submitted (14-JUN-2001)
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Lightfoot, S.A.,
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21673987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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Mammalia; Eutheria;
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nas.J.S., Hocker,J.R., Lerner,M.R., Brackett,D.
ghtfoot,S.A., Hanas,R.J., Maduhadson,K. and Mor
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/protein_id="AAL69685.1"
/protein_id="AAL69685.1"
/db_xref="GI:18448380"
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/db_xref="taxon:10116"
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Pred. No. 6.1e-145;
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Mammalia; Eutheria;
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CACATTGAACGCAAACATGGAAACCCACAAAAAACAGTATGTGTGCAGTTATGAGGGTTGC 190
                                                                                                                     CATTITGAACGCAAAACATGAAAATCAACAAAAACAATATATATGCAGTITITGAAGACTGT
                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLLL at: http://image.lln Series: IRAK Plate: 65 Row: 1 Column: 4
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akhter, N., Ayelé, K., Beckström-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Ö.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaithersburg, Maryland;
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nilarity 78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                  Score 560.6; Pred. No. 1.3e
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1.3e-115;
hes 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTATGCCGGAAAAACATTTAAACGCAAAGATTACCTTAAGCAACACACATGAAAACTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTTGGCCTCTCGCCTCAGTGGGTACTTCCCTCCTAAGAGGAAACAAGAGCCCGACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGGCATGGGAAAGTTCACGAGGGCTACCTGTGTCAAAAGGGATGTTCTTTCATGGGA
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                           Direct Submission
Submitted (03-FEB-2000) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
                                                                               Waterston, R
                                                                                            Submitted (23-MAY-1998) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, 3 (bases 1 to 97979)
                                                                                                                                         Waterston, R.
Direct Submission
                                                                                                                                                                           The sequence of Homo sapiens Unpublished 2 (bases 1 to 97979)
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 97979)
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 Center:
Washington University Genome Sequencing Center
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Missouri 6
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Missouri 63108,
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                                                                                                            USA
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Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc and

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For furth details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc. VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is
actual end is at base position 97' http://www.genomesystems.com). For further γď

is at base position 1 of 97979 of RP4-531G15.

RP4-531G15;

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FEATURES
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rpt_family-"(CA)n"
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/rpt_ 14415

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12888. 13001
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42711. .43026
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17465. .17685
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16041. .16362
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15648. .15729
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14264. .14417
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19508. .19692
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18630. .18750
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5. .32515
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               _family-"L1"
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51739. .517ac
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48067. .48494
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43847. .44539
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43552. .43886
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52362. .52665
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47673. .48037
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46091. .47111
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45246. .45667
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45132. .45245
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/rpt_fami 19702. .19

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/rpt_f. 7rpt_1 7rpt_ta 30338.

repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature repeat_region repeat_region repeat_region repeat_region repeat_region

/rpt_famil

/rpt_fam1 32940. .3

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TITLE
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Best Local Similarity 76.8
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Submitted (05-MAY-1999) Genome Sequen
University School of Medicine, 4444 F
MO 63108, USA
On May 5, 1999 this sequence version
Location/Qualifiers
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Homo sapiens clone NH0547G15,
AC006045
AC006045.2 GI:475277
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Submitted (22-NOV-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Unpublished
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             ATTCAACACAAAATCAAACTTGAAGAAACATTTTGAACGCAAACATGAAAATC
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/db_xref="taxon:9606"
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Bielicki,L., Haakenson,W. and
The sequence of Homo sapiens
Unpublished (2001)
3 (bases 1 to 111722)
Waterston,R.H.
                                                                                                                                                                   Homo sapiens
AC074390
AC074390.6 G
                                                                             1 (bases 1 to 111722)
Sulston, J.E. and Waterston, R.
Toward a complete human genome
Genome Res. 8 (11), 1097-1108 (
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates;
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RP11-515K14
                                       and
                               BAC clone
                                                                                                                  Craniata; V
Catarrhini;
                                                                               (1998)
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from DNA

7,

complete linear

sequence PRI

21-FEB-2002

Vertebrata;

Euteleostomi;

Hominidae;

RP11-515K14

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TAAAGATCAAAGTAAAGCTATCTTCTGAAAAATGAAATTTGGCCTCTCATCTCAGT-AAA
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FEATURES SOURCE		TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is CTD-2105K18, 2000 bp overlap; the clone sequenced to the right is RP11-533K11, 2000 bp overlap. Actual start of this clone is at base position 141753 of CTD-2105K18; actual end is at base position 16829 of RP11-533K11. Polymorphisms have been identified between AC016444 and AC074390. Data from AC016444 was used to finish this clone, AC074390. Location/Qualifiers 1. 111722 //organisms"Homo sapiens" //db_xref="taxon:9606" //chromosome="7" //map="7" //map="7" //clone="RP11-515K14"	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone: and the assembly was confirmed by sequence from covered of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McDherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries, Genomics Si:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org	Direct Submission Submitted (30-UUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 111722) Waterston, R. H. Direct Submission Submitted (19-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 111722) Waterston, R. Direct Submission Submitted (21-FBB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 19, 2002 this sequence version replaced gi:17976493
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           TGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGT
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29167. .29194
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3E 2 (bases 1 to 206622)
3E Birren, B., Linton, L., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanilan, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                   Submitted (26-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced gi:6778507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 11 clone RP11-384I14 map 11, SEQUENCE, 16 unordered pieces.
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Contact: sequence_submissions@genome
------- Project Information
Center project name: L5006
Center clone name: 384_I_14
                                                                                                               Center: Whitehead Institute/ MIT Center code: WIBR
                                                                                       Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16188 16287: gap of 100 bp 16288 18728; gap of 100 bp 18629 18728; gap of 100 bp 18729 22545; contig of 3817 bp 22546 22635; gap of 100 bp 22546 27333; contig of 4688 bp 27334 27433; gap of 100 bp 27334 27433; gap of 100 bp 27334 27438; contig of 5285 bp 32719 32819; gap of 100 bp 32819 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 37976 38075; gap of 100 bp 379
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127925 128024:
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Consensus quality: 190829 bases at least Q40 consensus quality: 198597 bases at least Q30 Consensus quality: 202013 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 4.2 in Q20 bases; agarose-fp Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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13593 14758: contig of 1166
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14859 16187: contig of 1329
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27434. .32718
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16288. .18628
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14859. .16187
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22646. .27333
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18729. .22545
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/db_xref="taxon:9606"
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58135: contlg of 9
9235: gap of 10
69592: contla of 1
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AAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTTAATCTCCAAAGCCATATCCTCTC
                                  --ATTATCTTAAGCAACATATGAACACTCATGCCCCAGAAAGGGATAT-TTTTGACATAC
                                                                  GAGAGAAACTTATAAAAAAGGAAACAACATATGAAGCAGGCCAGAAAACATTTAAAC----
                                                                                                                                                                           TATATGTCAAAAAGCGTGTTCTTTTGTGGTGAAAGCATGAACAGAAGTTTTGAAAACATGT
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32819. .37975
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48160. .58135
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On Jan 28, 2001 this sequence version replaced gi:12580980.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is annotated repeat sequence elements using the 'unsure' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCAGAGTAATA 37138
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                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr9
RP11-575C20 is from the library RPCI-11.2
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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1 (bases 1 to 199517)
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                                                                                                                                                                                                                                                               sequence is the entire insert of clone RP11-575C20 The true end of clone RP11-279E1 is at 116738 in this sequence. The right end of clone RP11-21817 is at 84470 in this sequence
                                                                                                                                                                                                                                                                                                                                                              //www.chori.org/bacpac/home.htm
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/note="Single clone region.
restriction digest data."
159357. .159427
                                                                                                                         /clone="RP11-575C20"
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/chromosome="9"
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                                                        ACATGATCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGAG 1074
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                          ATACCATTGCAACAAGAAGAAAATTAAACTCAGAGTAAAACCGAGCTCATGAAAAAACGGAG
                                                                                                                                                                ACATGCTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GCACTAGTGGCTGTGACAGAAAATTCAACACAAAATCAAACTTGAAGAAATATTTT 124246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGCAGCCACTGGCTGATCAAAAATTCAACACAAAATCAAAACTTGAAGAAACATTTT
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Compositions and methods
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SUMMARIES

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71.1	71.8	72.4	74.5	75.8	76.0	Query Match
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9 AL574318	BM562682	AL555777	AL550467	AL518337	BM553401	Length DB ID
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ALIGNMENTS

FEATURES Source	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BM553401 LOCUS
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1968 row: o column: 07 High quality sequence stop: 673. Location/Qualifiers 11078	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1078) NIH-MGC http://mgc.nci.nih.gov/.	72564 NIH_MGC_41 uence. GI:18792097	BM553401 1078 bp mRNA linear EST 20-FEB-2002

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AACTTCTG-AACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGGAGTATGCCGGA
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/tissue_type="mmelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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1 (bases 1 to 958)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
http://fulllength.invitrogen.com"
                                                                                                                                                                                                                   /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="CS0DA009Y018"
/clone_1ib="LTI_NFL011_NBC1"
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/lab_host="DH10B"
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Contact: Genoscope
Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, v
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Location/Qualifiers
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http://fulllength.invirtogen.com"
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/clone="cS0D1057YN01"
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Pred. No. 4.2e-190;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 881)
                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National
BP 191 91006 EVRY cedex - Fa
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AL555777 LTI_NFL006_PL2
prime, mRNA sequence.
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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AGENCOURT_6588903 NIH_MGC_98
5', mRNA sequence.
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         Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1059)
NIH-MGC http://mgc.nci.nih.gov/.
wational Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                   Homo sapiens
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  cgapbs-r@mail.nih.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1998 row: a column: 24
High quality sequence stop: 717.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@enoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Eutheria;
1 (bases 1 to 937)
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 Conservative
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/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
bttp://filliosephiifetech.com URL:
                                                                                          http://fulllength.invitrogen.com"
198 c 204 g 321 t
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/db_xref="taxon:9606"
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Score 862.8;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                              TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
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                                                                                                                                                                        CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
                                                                                                                                                                                                  CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
                                                                                                                                                                                                                                                                              TGCAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2478 row: j column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="hepatocellular carcinoma, cell line"
/lab host="0H10B (phage-resistant)"
/note="Organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CONA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

16 a 212 c 200 g 201 t 1 others
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/clone="IMAGE:6283123"
/clone_lib="NIH_MGC_100"
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Li,W.B., Gruber,C., Jessee,J
Full-length cDNA libraries a
Unpublished (2001)
Contact: Genoscope
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Location/Qualifiers
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                                                                                            /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                        http://fulllength.invitrogen.com"
240 c 227 g 206 t
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/clone="CSODC024YE05"
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1; Mismatches 7;
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                                                           TATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCA 570
                                                                                                                                                                                                          CACAAAATCAAACTTGAAGAAACATTTTGAASGCAAACATGAAAATSAACAAAAASAATA
                      AAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAAACATGTGAGAGAAAAC
                                            TATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCA
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AL574698 LTI_NFL006_PL2 H
AL574698 LTI_NFL006_PL2 H
prime, mRNA sequence.
AL574698
AL574698.1 GI:12935148
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 906)
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//clone_lib="LTI_NFL006_PL2"
//tissue_type="placenta"
//note="vector: pcMvSpORT 6; Site_1: NotI: 1st strand cDNA
//note="vector: pcMvSpORT 6; Site_1: NotI: 1st strand cDNA
//note="vector: pcMvSpORT 6; Site_1 five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Rv sites of the pcMvSpORT 6
vector: Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
96 a 173 c 199 g 309 t 29 others
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/db_xref="taxon:9606"
/clone="CS0DI065YI23"
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                                                                                                                                                                                                                                                                                                                                                                                69.6%;
95.1%;
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                                                                                                                                                                                                                                                                                                                                                                               Score 844.6; DB 9;
Pred. No. 6.1e-177;
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                                                                                                                                                                                                                                                                                          Genomics Laboration Helix Research Institute
Helix Research Institute
Kisarazu, Chiba
                                                                                                                                                                                                                                                                                                                                                                                                                          Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 893)
                                                                                                                                                              Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                  Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                     HRI human cDNA project
Unpublished (2000)
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Tel: 81-438-52-3975
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HEMBAl Homo sapiens
                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1002055"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
                                                                                                                                                 Location/Qualifiers
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   BQ644275 902 LAGENCOURT_8355851 NIH_MGC_100 5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2484 row: j column: 14
High quality sequence stop: 642.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
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NIH-MGC http://mgc.nci.nih.gov.
National Institutes of Health,
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Eukaryota; M
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a 208 c
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
LIRT (Life Technologies). Note: this is a NIH_MGC
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/clone="IMAGE:6285421"
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Pred. No. 4.9e-175;
0; Mismatches 12;
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AL578193
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EST.
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Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.gen
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 933)
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                          /note-*Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
          http://fulllength.invitrogen.com"
192 c 207 g 326 t
                                                                                                           /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6;
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/db_xref="taxon:9606"
/clone="cs00K002YJ18"
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     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 1089)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMA044 row: f column: 22

High quality sequence stop: 610.
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999
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/lab_host="DBHOB (phage=resistant)"
/note="organ: breast; Vector: pcTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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plate: L/cM1810 row: d column:
High quality sequence stop: 880.
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                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/clone=TinAGE:4906710"
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/tissue_type="epithelioid c
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Size-selected >50bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library. | "
Note: this is a NH_MGC Library. | "
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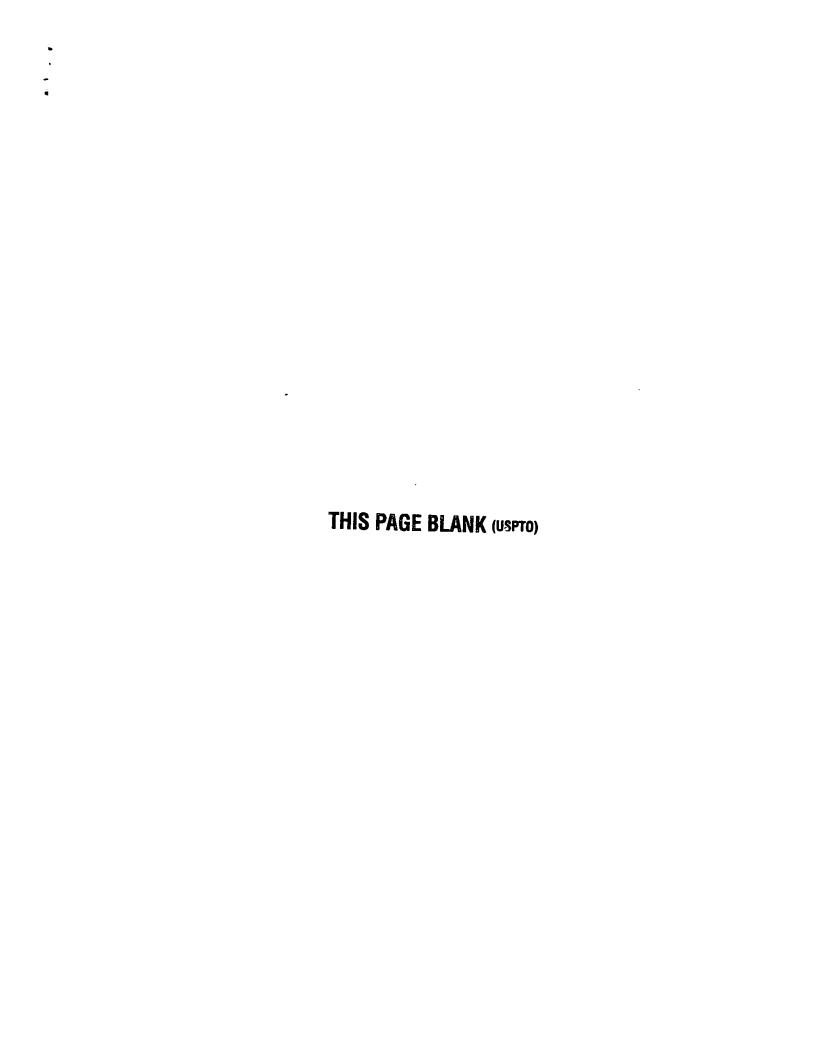
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   TGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2449 row: f column: 19
High quality sequence stop: 608.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 908)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93217, 87.3 391 5 US-09-724-676A-93216 Sequence 93217, 87.3 391 5 US-09-724-676A-93218 Sequence 93218, 87.3 391 5 US-09-724-676A-93219 Sequence 93219, 87.3 391 5 US-09-724-676A-93220 Sequence 93219, 87.3 391 5 US-09-724-676A-93221 Sequence 93221, 79.4 354 5 US-09-724-676A-93221 Sequence 93222,	>	93224,		US-09-72		. 4	1595	38
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93217, 87.3 391 5 US-09-724-676A-93219 Sequence 93218, 87.3 391 5 US-09-724-676A-93219 Sequence 93218, 87.3 391 5 US-09-724-676A-93220 Sequence 93220, 87.3 391 5 US-09-724-676A-93220 Sequence 93221,	➣	93222,		us-09-72		. 4	1595	37
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93214, 87.3 391 5 US-09-724-676A-93216 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93217, 87.3 391 5 US-09-724-676A-93218 Sequence 93218, 87.3 391 5 US-09-724-676A-93219 Sequence 93218, 87.3 391 5 US-09-724-676A-93220 Sequence 93220,	>	93221,		US-09-72		·w	1752	36
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93216, 87.3 391 5 US-09-724-676A-93217 Sequence 93216, 87.3 391 5 US-09-724-676A-93218 Sequence 93218, 87.3 391 5 US-09-724-676A-93219 Sequence 93219,	⋗	93220,		_		'n	1752	35
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93216, 87.3 391 5 US-09-724-676A-93217 Sequence 93217, 87.3 391 5 US-09-724-676A-93218 Sequence 93218,	⊳	93219,		۵		'n	1752	34
87.3 391 5 US-09-724-676A-93213 Sequence 93213, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93214, 87.3 391 5 US-09-724-676A-93216 Sequence 93216, 87.3 391 5 US-09-724-676A-93217 Sequence 93217,	⋗	93218,		_		W	1752	33
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93215, 87.3 391 5 US-09-724-676A-93216 Sequence 93216,	➣	93217,		_		'n	1752	32
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214, 87.3 391 5 US-09-724-676A-93215 Sequence 93215,	⋗	93216,		_		w	1752	31
87.3 391 5 US-09-724-676A-93213 Sequence 93214, 87.3 391 5 US-09-724-676A-93214 Sequence 93214,	≻	93215,		_		W	1752	30
87.3 391 5 US-09-724-676A-93213 Sequence 93213,	×	93214,		_		'n	1752	29
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87 3 301 5 He-00-704-676-03001 common 03001	>	93221,	Sequence	5 US-09-724-676-93221			1752	27

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FERKHENQQXQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLK
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              HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
                                                                   PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
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HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
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Pred. No. 4e-176;
1; Mismatches
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US-09-724-676-93234

Sequence 93234, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spling of CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93234
LENGTH: 430
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93223
LENGTH: 430
Type: PAT
ORGANISM: Homo sapiens
US-09-724-676-93223
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                                                                    ; TYPE: PRT; ORGANISM: Homo sapiens
US-09-724-676-93234
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                       Query Match
Best Local Similarity
Matches 363; Conserv
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Best Local Similarity 99.5%;
Matches 363; Conservative
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                                 99.5%;
                     Score 2000; DB 5
Pred. No. 4e-176;
1; Mismatches
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Pred. No. 4e-176;
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Sequence 93245, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93245
LENGTH: 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-09-724-676-93245
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Matches 363; Conserv
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HDPDKKKMKLKVKKSREKRSLASHLSGY IPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
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Pred. No. 4e-176;
1; Mismatches
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RESULT 5
US-09-724-676-93256
US-09-724-676-93256
Sequence 93256, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93256
LENGTH: 430
TYPE: PRT
ORGANISM: Homo sapiens
                                                            APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93267
LENGTH: 430
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Pred. No. 4e-176;
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US-09-724-676-93278

Sequence 93278, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative spl

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CÜRRENT FILING DATE: 2000-11-28

NUMBER OF SEO ID NOS: 97222

SOFTWARE: PALENTIN version 3.2

SEQ ID NO 93278

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Sequence 93300, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93300
LENGTH: 430
TYPE: PRT
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US-09-724-676-93300
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Best Local Sim
Matches 363;
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93289
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Sequence 93212, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93212
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US-09-724-676A-93212
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TYPE: PRT
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363; Conservative
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Pred. No. 4e-176;
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Pred. No. 4e-176;
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APPLICANT: Compugen LTD:
TITLE OF INVENTION: Variants of alternative sp:
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93223
LENGTH: 430
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        Sequence 93234, Application US/09724676A
GENERAL INFORMATION:
APPLICANY: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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Matches
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NUMBER OF SEQ ID
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Pred. No. 4
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93245
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SEQ ID NO 93234
LENGTH: 430
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 363; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                     LENGTH: 430
TYPE: PRT
ORGANISM: Homo:
186
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                                                   LCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAANGCDQKFNTKSNLKKH
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Pred. No. 4e-176;
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Pred. No. 4e-176;
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Sequence 93256, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93256
              RESULT 15
US-09-724-676A-93267
Sequence 93267, Application
GENERAL INFORMATION:
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US-09-724-676A-93256
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93256
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Matches 363;
APPLICANT: Compugen
TITLE OF INVENTION:
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                                                                                           VLTLG 365
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Variants
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CURRENT FILING NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93267
LENGTH: 430
TYPE: PRT
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Best Local
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Local Similarity 99.5%;
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VLTLG
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                                                                 HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
                                                                                                                      PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
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Search completed: February 10, 2003, 17:50:24 Job time : 42 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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414.5	421	425	453	563.5	821	1933	2000	2008	Score
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22	22	22	2 1	22	23	17	22	21	В
AAM79998	AAM79299	AAM80283	ARG09347	AAR85422	ABP41846	AAR91305	AAG75181	AAY93317	ID
Human protein SEQ	Human protein SEQ	Human protein SEQ	Novel human diagno	Amino acid seguenc	Human ovarian anti	Transcription fact	Human colon cancer	A human transcript	Description

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
	384.5	384.5	384.5	385.5	385.5	386	386.5	387.5	388.5	391.5	392.5	392.5	393	393	393	393.5	394.5	394.5	395	395.5	395.5	396	396.5	398.5	403	404	404	404	405	406.5	406.5	410.5	410.5	410.5	410.5
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	613	386	357	1520	577	406	759	1252	817	632	570	547	799	702	489	751	809	727	803	1050	412	577	646	773	934	779	779	779	1241	700	403	652	632	631	622
	22	22	22	22	23	22	23	22	22	22	22	22	21	23	22	22	22	22	22	22	21	22	23	22	22	22	22	22	22	22	22	22	22	22	22
ALTGNMENTS	AAB95862	AAM93303	AAB93635	ABG27130	AAE14680	AAU16023	AAU78844	AAM79739	AAM40475	ABG19011	AAM79350	AAM78366	AAB21003	ABB04333	ABB50238	AAM39508	AAM38689	ABG16954	AAB95278	ABG09685	AAY93316	AAM93698	ABP51377	AAM41294	ABB69958	AAM79958	AAM78974	ABG00880	ABG02797	AAM40001	53	AAM79171	ABG18386	993	AAM78947
	Human protein sequ	Human polypeptide,	Human protein sequ		_	_		_	3		protein	protein	Human nucleic acid	_	_	_	7		_	Novel human diagno	A transcription fa	Human polypeptide,		Human polypeptide	phila me	-	_			Human polypeptide	phila me	Þ	human di	protein	. Human protein SEQ

ALIGNMENTS

RESULT 1
AAY93317
ID AAY9

AAY93317 standard; Protein; 365 AA

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WPI; 2000-387419/33.
N-PSDB; AAA15405.
                                                                                                                                                                           cancer.
                                                                                                                                                                                   Human; transcription factor; htfIIIA; DNA-binding protein; transcription; ribosomal RNA 5S gene; transcriptional control;
                                                                                                                                                                                                            A human transcription factor designated htfIIIA.
                                                                                                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                 AAY93317;
                                                                                                      09-NOV-1999;
                                                                                                                                                          Homo sapiens.
                                                  Bordon-Pallier F,
                                                                   (HMRI ) HOECHST MARION ROUSSEL
                                                                                     10-NOV-1998;
                                                                                                                       18-MAY-2000.
                                                                                                                                        WO200028024-A1
                                                                                                                                                                                                                              (first entry)
                                                                                     98FR-0014146.
                                                                                                      99WO-FR02738
                                                  Rocher C;
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New nucleic acid encoding human transcription factor IIIA, useful for treatment and diagnosis of cancer and inherited disease

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Matches 365
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           29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                 Human colon cancer antigen protein SEQ ID NO:5945
                                                                                                                                                                                       03-SEP-2001
                                                                                                                                                                                                                                  AAG75181 standard;
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                                                                                                            Homo
                                                                                                                                 colorectal carcinoma;
                                                                                      WO200122920-A2
                                           28-SEP-2000; 2000WO-US26524
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                                                                                                            sapiens
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                                                                                                                                            colon cancer;
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llarity 100.0%;
Conservative C
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           99US-0163280
                     99US-0157137
                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                     entry)
                                                                                                                                  colon cancer antigen; chromosome 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents a human
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAP7789 represent sequences used in the exemplification of the
                                           AAR91305 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                AAR91305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for
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                                                                                                                                              VLTLG
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                                             Protein;
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diagnosing
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and/or treating colorectal cancers -
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07-JUL-1996

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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HDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
                                                                                                                PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
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                                         HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
                                                                                          PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
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96.2%;
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Pred. No. 5.5e-153;
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RESULT 4
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP42328) and to cDNAs encoding them (ABQ54311-ABQ56305), and also compasses polypeptides 90% identical and polynucleotides 95% identical CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen CC polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, cc treating, prognosing or preventing various ovary and/or breast-related CC disorders. Such conditions include ovarian concer and breast cancer, and cc disorders (e.g., infertility, disorders of pregnancy, anovulation, collisorders, infections (e.g., chiamydia, HIV, toxoplasmosis, and toxic concers syndrome), inflammatory conditions (e.g., mastitis, ophoritis and commune disorders (e.g., congenital and acquired immunedisorders (e.g., anaemia), cardiovascular disorders, crespiratory disorders, neurological disorders, gastroIntestinal disorders cand urinary system disorders. Ovarian antigen polypeptides and cc further be used for gene therapy, chromosome mapping, in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID No 2978; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
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The invention relates to a nucleic acid (NA) binding polypeptide (I) comprising a repressor domain and several NA binding domains (BDs) l by at least one non-canonical linker. (I) may be used to identify NA a complex mixture, to differentiate single back and the complex mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                 Nucleic acid binding polypeptide, used to identify nucleic acids and treat inflammatory, neurological, and dermatological disease, compris a repressor domain and several nucleic acid binding domains linked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid binding polypeptide; repressor domain; cardiant; nootropic; circulatory active; anti-inflammatory; dermatological; neuroprotective; cerebroprotective; antibacterial; antifingal; antiviral; antirheumatic;
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                                                                                                                                             Claim 31;
                                                                                                                                                                                                non-canonical linker(s)
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N-PSDB; AAH23370.
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30-MAY-2000; 2000GB-0013102
30-MAY-2000; 2000GB-0013103
30-MAY-2000; 2000GB-0013104
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Pred. No. 1.1e:
1; Mismatches
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No. 1.1e-60;
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   diagnostics, responsible
New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to
                                                                                                                                                                               31-MAR-2000;
                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                       11-OCT-2001
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food supplement; medical imaging; diagnostic; genetic (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTGEKPFYCAATGCDQKFNTKSNLKKHFERKHENQOKQYICSFEDCKKTFKKHQQLKIHQ
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                                                                                                       RT,
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2000US-0649167.
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Pred. No. 4.2e-39;
Pred. no. 4.2e-39;
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                                                                                                                                                                                                                                                                                                                                        forensic;
                  mutations
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RESULT 7
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Best Local :
           03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haemator
                                                                                                                                                                                                                                                                                                                                                       Human protein SEQ ID NO 3929.
                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM80283 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                    05-FEB-2001;
                                                                                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                                W0200157190-A2
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                           nervous system disorder; arthritis;
                                                                                                                                                                                                                                                                                             tissue growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 HEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIP 330
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87; Conserv
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           2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-06633561.
2000US-06633561.
2000US-0728422.
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                                                                                                                                                    2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                             factor;
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                                                                                                                                                                                                                                                                                             immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   927
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Pred. No. 2.4e-30;
1; Mismatches 7;
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                                                                                                                                                                                                                                                                             inflammation
                                                                                                                                                                                                                                                                                             cancer; leukaemia
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from WIPO
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                                                                                                                                                                                                                                                                                                                     therapy;
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RESULT 8 AAM79299

DEXTX

06-NOV-2001

(first entry)

AAM79299;

AAM79299 standard;

Protein; 869

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Human protein SEQ ID NO 1961

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Matches 116; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C,
Zhao QA, Wang D,
Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
N-PSDB; AAK53416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AAM80020) are omitted as
                                                                                                                                                                                                                                                                                                                                  62 CKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVC---------
                                                                                                                                                                                                                                                                                                                                                                                             3 PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL
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                                                                                                                   GEKPYECLECGKSFGHSSTLIKHQR-THLREDPFKCPVCGKTFTLSATLLRHQRTHTGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80020) are omitted as the relevant pages from the sequence listing missing at the time of publication.
                                                        PY-KCPE--CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
                                                                                     DVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDP
                                                                                                                                                                                                    HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV------AKTWF
                                                                                                                                                                                                                                                                                                      RIHTGERPNTC - - SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT
                                                                                                                                                                              HTGEKPYKCPE--CGKRFGQNHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT
                                                                                                                                                                                                                                                                                                                                                                  PPVVPANEPSLRELVQG------RPAGAEKPYICN--ECGKSFSQWSKLLRHQ 227
                                                                                                                                                                                                                                          HTGEKPYKCTECEKAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT
                                                                                                                                                                                                                                                                      -----AATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Records for SEQ ID NO 2110 (AAK52581),
514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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, Wang J, Zh
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%; 32.0%;
                                                                                                                                                 ---ELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPER
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T. Zhang Gor
                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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lang J, Ren
Goodrich R
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           e 425; DB 22;
. NO. 9.1e-27;
ismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V, Zhou
Ren F, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2111 (AAK52582) and 3666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            927;
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                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
Zhao
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                               Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 4372-4374; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like
                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-2000;
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                           Inflammation.
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                            156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 YT,
O QA,
                                                                                                                          HTGEKPYKCPE--CGKRFGONHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-476283/51.
DB; AAK52432.
                          HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-----AKTWT
                                                   HTGEEPYKCTECEIAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT 283
                                                                                                         RIHTGERPNTC--SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT 227
                                                                                                                                                               PPVVPANEPSLRELVQG------
                                                                                                                                                                                       PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL 61
                                                                                                                                                                                                                                 Similarity
                                                                    ----AATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis and
                                                                                                                                                                                                                                                                       869 AA;
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2000US-0560875
2000US-0598075
2000US-0620325
2000US-0654936
2000US-06533561
2000US-0693325
2000US-0728422
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Wang J,
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Wejhrman T,
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, Zhang J, Ren
n T, Goodrich F
                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                Score 421; DB 22;
Pred. No. 1.8e-26;
1; Mismatches 116
                                                                                                                                                             RPAGAEKPYICN -- ECGKSFSQWSKLLRHQ 169
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F, C
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from
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                                                                                                                                                                                                                                          Length 869;
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the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities
                                                                                                                                                                                                                                                                                                                                                    arthritis and
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                                                                                                                                                                                                                  ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZW;
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RESULT 9
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                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                              Tang
Zhao
                                                                                                                                                                              Claim 20; Page 4019-4021; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human: cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM79014 standard;
                inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581),
                                         treatment of cancer, leukaemia,
                                                                                                                                                                                                         useful in
                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein SEQ ID NO 1676.
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Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK(AAM80020) are omitted as the relevant pages from the
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DB; AAK52147.
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2000US-0560875.
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Wang J, Zh
Wejhrman T,
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, Zhang J, Ren
n T, Goodrich R;
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                                         nervous system disorders,
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0663355.

20-OCT-2000; 2000US-0728422.
                  Tang
Zhao
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               Liu C,
Wang D,
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                  RT, Asundi V,
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                  Zhou
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Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematop tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                     06-NOV-2001
                                                                                                                                                                       AAM78947 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 29.1 les 111; Conservative
                                                                                                                                                                                                                                                                                                                             KGHSIT-HLSTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSRCPISSCNKLFTS
                                                                                                                                                                                                                                                                                                                                                              QSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH--DPDKKKMKLKV----KKSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHLCKHT---GERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKS 115
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)B; AAK53131.
                                                                                                                                                                                                                                                           KHSMKTHM - - - - VKRHKVGQDL
                                                                                                                                                                                                                                                                                           KRSLASHLSGYIPPKRKQGQGL 339
                                                                                                                                                                                                                                                                                                                                                                                                KLLRH------KRK------HDDDRRF-MCPVEGCGKSFTRAEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFSHNRAHFREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCDFDGCGWNFTSMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLKAHMKGHEQENSFKCEVCEESFPTQAKLGAHQRSHFEPERPYQCAFSGCKKTFITVSA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Page 404-405; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904 AA;
                                                                                                   (first entry)
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                                                                                                                                                                       Protein;
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Pred. No. 6.6e-26;
7; Mismatches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy
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                                 gene therapy;
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Best Local S
Matches 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang
Zhao
                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy -
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27-APR-2000;
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19-JUL-2000;
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429
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20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
                           248
                                                       373
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                                                                                                                                                                                                                                                                                Local Similarity 30.
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                                                                                                                                                                 YKCEECGKAFNQSSTLTKHKKIHTGEKPYKCEECGKAFNQSSTLTKH--KKIHTGEKPYV 316
C--EECGKAFVASSTLSKHEI-IHTGKKPYKCEE--CGKAFNQSSSLTKHKKIHTGEKPY
                        CPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-
                                                                      CQK-GCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCR
                                                                                                           C--EECGKAFKYSRILTTHKRIHTGEKPYKCNK--CGKAFIASSTLSRHEFIHMGKKHYK 372
                                                                                                                                                                                                                         YICE--ECGKAFKYSSALNTHKRIHTGEKPYKCD--KCDKAFIASSTLSKHEIIHTGKKP
                                                    CEECGKAFI---WSSVLTRHKRVHTGEKPYKCEECGKAFKYSSTLSSHKRSHTGEKPY-K 428
                                                                                                                                    CSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YV 190
                                                                                                                                                                                                                                                  FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
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Wang D,
Yang Y,
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2000US-0620325.
2000US-0654936.
2000US-0663561.
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2000US-0560875
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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                                                                                                                                                                                             -----CDQKFNTKSNLKKHFERKHENQQKQYI 133
                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                             Score 410.5; DB 22; pred. No. 8.9e-26; 48; Mismatches 137;
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Ren F, Chei
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from
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the sequence listing
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R, Wang
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                                                                                                                                                                                                                                                                                63;
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                           Tang YT,
Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene vaccine; peptide therapy; stem cell growth factor; haematopoiesi: tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                      Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                              Claim 20; Page 388; 6221pp; English.
                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities.
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                                                                 inflammation
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DB; AAK53064.
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Yang Y,
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2000US-0560875.
2000US-0598075.
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2000US-063325.
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Wejhrman T,
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, Zhang J, Ren F, Cher
n T, Goodrich R;
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from
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the sequence listing
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R, Wang
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Query Match Best Local S Matches 109

al Similarity 109; Conserv

Conservative

20.4%;

Score 410.5; Pred. No. 9.16 48; Mismatches

.1e-26; DB 22;

Indels

63.

Gaps

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Length

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                    Claim 20; SEQ ID No 48745; 103pp; English.
                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                           diagnostics, forensics, responsible for genetic biodiversity
                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #18377.
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                                                                                                                                                                                                                                                                                                         2001-639362/73
DB; AAS82573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C--EECGKAFVASSTLSKHEI-IHTGKKPYKCEE--CGKAFNQSSSLTKHKKIHTGEKPY 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C--EECGKAFKYSRILTTHKRIHTGEKPYKCNK--CGKAFIASSTLSRHEFIHMGKKHYK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKCEECGKAFNQSSTLTKHKKIHTGEKPYKCEECGKAFNQSSTLTKH--KKIHTGEKPYV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEECGKAFI - - - WSSYLTRHKRVHTGEKPYKCEECGKAFKYSSTLSSHKRSHTGEKPY - K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQK-GCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YICE--ECGKAFKYSSALNTHKRIHTGEKPYKCD--KCDKAFIASSTLSKHEIIHTGKKP
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                                                                                                                                                                                                                                                                                                                                                           RT,
                                                                                                                                                                                                                                                                                                                                                                                            HYSEQ
                                                                                                                                                                                                                                     polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                        Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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RESULT 14
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ID AAM79
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Best Local
 03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00017 expresent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM79171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                               05-FEB-2001;
                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                           WO200157190-A2
                                                                                                                                                                                                                                                          nervous system disorder; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                      Human protein
                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                      AAM79171;
                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCEECGKAFNQSSSLTKH-----KKIHTGEKPYKCEECGKAFNQSSTLIKHKKIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQK-GCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKCEECGKAFNQSSTLTKHKKIHTGEKPYKCEECGKAFNQSSTLTKH--KKIHTGEKPYV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVCAATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C--EECGKAFVASSTLSKHEI-IHTGKKPYKCEE--CGKAFNQSSSLTKHKKIHTGEKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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                                                                                                                               2001WO-US04098
                                                                                                                                                                                                                                                                                                                                       SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CDQKFNTKSNLKKHFERKHENQQKQYI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 9.1e-
B; Mismatches
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                                                                                                                                                                                                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemarcopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity individual in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xue
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Zhao
               Drosophila melanogaster
                                          Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                        Drosophila melanogaster polypeptide SEQ
                                                                                                                       26-MAR-2002
                                                                                                                                                                                  ABB64531 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 4219-4221; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                              599
                                                                                                                                                                                                                                                                                                                      543
                                                                                                                                                                                                                                                                                                                                                                                  486
                                                                                                                                                                                                                                                                                                                                                                                                               166
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                                                                                                                                                                                                                                                                                        281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                            E--CGKAFNWSSSLTKHKIIHTGEK
                                                                                                                                                                                                                                                                                                                                                                                                            QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETHKEEIL--CE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                        HAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                                                                                                 VCRKTFKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-476283/51.
DB; AAK52304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECGKAFTWSSSLNKHKRIHTGEKPYTC -- EECGKAFYRSSHLAKHKRIHTGEKPYTCEE - 431
                                                                                                                                                                                                                                                                                                                     ECGKAFTRSTALNEHKKIHSGEKPY-KC--KECGKAYNLSSTLTKH-KRIHTGEKPFTCE
                                                                                                                                                                                                                                                                                                                                                                               -EECGKAFIWSASLNEHKNIHTGEKPYKC-KECGKAFNQSSGLIIH-RSIHSEQKLYKCE 542
                                                                                                                                                                                                                                                                                                                                                                                                                                           -CGKAFNQSSTLILH-KRIHSG-QKPYKC--EECGKAFTRSTTLNEHKKIHTGEKPYKC- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Drmanac RT, Asundi V,
Wang D, Wang J, Zhang J, Ren
Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 AA;
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                                                                                                                      (first
                                                                                                                      entry)
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Pred. No. 9.5e-26;
1; Mismatches 111
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F, C
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from
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R, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Job time : 77 secs
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL30511), expressed DNA sequences (ABL18176-ABL30511) expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000;
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nes 105; Conserv
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                                                                                          KRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL 364
                                                                                                                           YLRNLRQHMLTAH-SGRRFECQALDCGRCFSSAQNLARHLLRDHKDGATKKELKAKKKDK
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                                                              SKTGEGGKTKSTSRKRRRDAGRS---
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                                                                                                                                                                                                                                                                                                                                                                                                               RFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHI-LTH---
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Copyright (c) 1993 - 2003
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US-08-523-376-3
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251.5 12.5 441 4 US-09-172-045-2 248 12.4 345 1 US-08-102-942h-2 248 12.4 345 4 US-09-037-179B-2 246 12.3 429 1 US-08-234-783-4 246 12.3 429 1 US-08-234-783-4 246 12.3 429 1 US-08-102-942h-4 243.5 12.1 449 1 US-09-102-942h-4 243.5 12.1 449 4 US-09-103-179B-4 242.5 12.1 449 4 US-09-234-32-11 242.5 12.1 449 1 US-08-102-942h-6 242.5 12.1 449 1 US-08-102-942h-6 242.5 12.1 449 1 US-08-103-719B-6 242.5 12.1 449 1 US-08-103-719B-6 242.5 12.1 449 1 US-08-103-115 242.5 12.1 449 1 US-08-103-116 253.6 11.9 33.8 4 US-09-234-613-4 254.5 11.2 671 3 US-09-121-321-16 254.5 11.2 671 3 US-09-121-321-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16 254.5 11.2 671 3 US-08-93-9303h-16	4 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29
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1 US-08-172-045-2 1 US-08-102-942A-2 2 US-09-037-179B-2 1 US-08-234-783-4 1 US-08-234-783-4 1 US-08-102-942A-4 5 PCT-US95-05523-4 1 US-09-124-2A-4 4 US-09-234-32-11 1 US-08-102-942A-6 2 US-09-234-32-11 1 US-08-102-942A-6 2 US-08-933-750C-4 4 US-09-234-613-4 3 US-09-121-321-16 3 US-09-121-321-16 5 PCT-US92-0640-2 1 US-08-933-803A-16 5 PCT-US92-0640-2	706	414	671	671	338	338	449	449	447	449	449	429	429	429	345	345	441
US-09-172-045-2 US-08-102-942A-2 US-08-234-783-4 US-08-234-783-4 US-08-102-942A-4 US-08-102-942A-4 US-08-102-942A-4 US-09-234-332-11 US-08-102-942A-6 US-09-037-179B-6 US-09-037-179B-6 US-09-037-179B-6 US-09-037-179B-6 US-09-037-179B-6 US-09-037-179B-6 US-08-033-150-4 US-09-033-150-16 US-09-121-321-16 US-09-121-321-16 US-09-121-321-16 US-08-933-803A-16 US-08-933-803A-16 US-08-933-803A-16 US-08-933-803A-16	1	Ç	4	ω	4	N	4	ب	ω	4	-	5	بر	一	4	_	4
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	Appl:	Appli	App1	Appl	Appl:	Appli	App1 i	App1 i	, Appl	Appli	Appli	App1 i	Appli	Appli	App1	Appli	Appli

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: TSUTOMU, FUJIWARA
APPLICANT: SATOSHI, TAKEDA
APPLICANT: VOSHIKAZU, SHIMADA
APPLICANT: KOUICHI, OZAKI
APPLICANT: Sadahito, SIN
TITLE OF INVENTION: hTFIIIA GENE
                                                                                                                                                                           ; TOPOLOGY: lir; MOLECULE TYPE: US-08-523-376-3
                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Applic
Patent No. 5808030
                                                                                                               Matches
                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2100 Pennsylvan
CITY: Washington
STATE: D.C.
COUNTRY: United States
                                                                                                                                                                                                                              TYPE:
                    61
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/523,376
                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                              LCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKH
                                                                                                              351;
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08523376
                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                        423 amino acids
                                                                                                               Conservative
                                                                                                                                                                                                           Linear
                                                                                                                                                                                          protein
                                                                                                                           96.3%;
                                                                                                            Score 1933; Di
Pred. No. 8.3e
3; Mismatches
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                                                                                                                                            Length 423;
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                                                                                                                                                     Query Match
Best Local S
Matches 93
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        TELEX: 649110 3 10: 10: SEQUENCE CHARACTERISTICS: LENGTH: 711 amino acids
                                                                                                                                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2100
CITY: Washington
STATE: D.C.
United (
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APPLICANT: TAKESHI, WATANABE
APPLICANT: WASATO, HORIE
APPLICANT: TOYOMASA, KATAGIRI
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
501 KPYEC--SDCGKTFTQKSHLNIH--QKIHTGERHHVCS--ECGKAFNQKSILSMHQRIHT
                                                                             445 KSYVCI--ECGQAFIQKAHLIVHQRSHTGEKPYQC--HNCGKSFISKSQLDIHHRIHTGE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419
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                                                                                                                                                     Local Similarity 32.9 hes 93; Conservative
                                          98 KPFVCAATGCDQKFNTKSNLKKHFERKHENOOKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
                                                                                                              38 RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHAKAHEGYVCQKGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt HDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA}
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                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08820170A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN GENE
                                                                                                                                                 19.0%; Score 381; DB 2; L 32.9%; Pred. No. 2.6e-30; tive 43; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KATAGIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/820,170A
                                                                                                                                                                                   Length 711;
                                                                                                                                                     Indels
                                                                                                                                                     28;
                                                                                                                                                   Gaps
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TELETAX: (40-, TELETAX: 6491103
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 711 amino acids TYPE: amino acids TYPE: amino acids TYPE: 11near 11near
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                                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-055-699 10
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                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TOYOMASA, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666
                                       555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKH-VRETH 213
214 KEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE--GCGRTYTTVENLQSHILSFH
                                                                       158 NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKH-VRETH 213
                                                                                                                                                                                          445 KSYVCI--ECGQAFIQKAHLIVHQRSHTGEKPYQC--HNCGKSFISKSQLDIHHRIHTGE 500
                                                                                                                                                                                                                                                                      Local Similarity 32.9
                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2100 Peni
CITY: Washington
                                                                                                                                                                                                                              38 RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                               KPYEC -- SDCGKTFTQKSHLNIH -- QKIHTGERHHVCS -- ECGKAFNQKSILSMHQRIHT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGERPYVCSE--CGKAFNNRSNFNKHQTTHTRDKSYKCSYSVK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-KMKLKVK 313
                                   GEKPYKCSE--CGKAFTSKSQFKEHQRIHTGEKPYVCTE-CGKAFNGRSNFHKHQITHTR
                                                                                                                                                KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERPFVCYKCGKAFVQKSELITHQRTHMGEK-----PYECLDCGKSFSKKPQLKVH-QRIH 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsutomu, FUJIWARA
Takeshi, WATANABE
Masato, HORIE
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US-09-273-565-10
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
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       GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING E
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Best Local Similarity 32.9
Matches 93; Conservative
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Patent No. 6166190
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TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-05
EARLIER FILING DATE: 1996-03-05
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FILE REFERENCE: Q-53599
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Query Match
Best Local Similarity
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/661,468
CURRENT FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
PRIOR PILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1997-03-05
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
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CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/273,565
PRIOR APPLICATION NUMBER: 09/273,565
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
; ORGANISM: Homo sapiens
US-09-661-468-10
                                                 SOFTWARE: Pa
SEQ ID NO 10
LENGTH: 711
TYPE: PRT
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SEQ ID NO 10
LENGTH: 711
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APPLICANT: WATANABE, TAKE
APPLICANT: HORIE, MASATO
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                                                                                                                                 PatentIn Ver.
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ilarity 32.9%;
Conservative 43
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SOFTWARE: PatentIn Ver.
SEQ ID NO 4
LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. 6451558
GENERAL INFORMATION:
APPLICANT: Cooke, Michael Paul
APPLICANT: Holness, Claire
APPLICANT: Sirenko, Oksana
TITLE OF INVENTION: No. 6451558el Genes in
FILE REFERENCE: 4.30629A/SYS
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Matches 93; Conser
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Best Local (
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                                                                                                                               SQGSSLFKHQRVHTGEKPFACPQCGRAFSHSSNLTQHQLLHTGERPF-RC--VDCGKAFA 453
                                                                                                                                                                                                                  FSHGSNLSQHRKIHAGGRPYACAQ--CGRRFCRNSHLIQHERTHTGEKPFVCAL-CGAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.6%; Score 353.5; DB 4; 31.5%; Pred. No. 1.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Mismatches 144; Indels
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US-08-475-844-9
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               GENERAL INFORMATION:
APPLICANT: Lobanenk
APPLICANT: Neiman,
APPLICANT: Klenova,
APPLICANT: Goodwin,
APPLICANT: Filippov
                                                                                                                                               Sequence 9, Application US/08475844 Patent No. 5972643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09063035 Patent No. 6160091
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20000
COMPUTER READABLE FORM:
CMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM AT-compatible, E
OPERATING SYSTEM: MS-DOS versi
SOFTWARE: WordPerfect version
CURRENT APPLICATION DATA:
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LENGTH: 803 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PEUKER APPLICANT: Martin
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                               509 RQFADPGALQRHVRIHTGEKPCQCVMCGKAFTQASSLIAHV-----RQHTGEKPYVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 SDPAACKAH-EKTH-SPLKPYGC--EECGKSYRLISLLNLHKKRHSGEARYRC--EDCGK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 SKAYGSVIHKC------EDCGKEFTHTGNFKRHIRIHTGEKPFSCRE--CSKAF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 RSVAGASSEGAPAKETE 527
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TYPE: amino acid
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ZIP: 20036
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                            KRKDYLKQHMKTHAPERDV-CRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETH--KEEILCEVCRKTF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGGGK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKF 111
                                                                                                                                                                                                                                                                                                                       KTFAMKQSLTRHAVVHDPDKKKMKLKVKKS-REKRSLASHLSGYIPPKRKQGQGLSLCQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFTTSGNLKRHQLVHSGEKPYQCDY-CGRSFSDPTSKMRHL-ETHDTDKEHKCPHCDKKF 455
                                                                                                                                                                                                                                                                                                                                                                  NOVGNLKAHLKIHIADGPLKCR----ECGKOFTTSGNLKRO-LRIHSGEKPYVCIH--CO 508
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                                      Klenova, Elena M.
Goodwin, Graham H.
Filippova, Galin
Collins, Steven
                                                                              Neiman, Paul E.
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                                                                                                       Lobanenkov, Victor V
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                   PCT-US95-08429-9
                                 RESULT 10
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Sequence 9, Application PC/TUS9508429
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LENGTH: 727 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/475,6
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,680
FILING DATE: 17-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CTCF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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CITY: San Francisco
STATE: CA
COUNTRY: USA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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REFERENCE/DOCKET NUMBER: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                          YALIOHOKSHKNEKRFKCDQCDYACRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLD 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPKPTKIKKKGVKKTFQCEL--CSYTCPRRSNLDRHMKSHTDERPHKCHL--CGRAFRTV 306
                                                                                           RKRKMRSKKEDSS 610
                                                                                                                              KYKKSREKRSLAS 323
                                                                                                                                                                   MHFKRYHDPNFVPAAFVC--SKCGKTFTRRNTMARHADNCAGPDGVEGENGGETKKSKRG
                                                                                                                                                                                                       SHILSFHEES - - - RPFVCEHAGCGKTFAMKQSLTRHA - VVHDPD - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG-----YVC-----QK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLLRNHLNTHTGTRPHKC--PDCDMAFVTSGELVRHRRYKH-THEKPFKCSM--CDYASV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFK 144
                                                                                                                                                                                                                                                                                                                    GTMKMHILQKHTENVAKFHCPHCDTVIARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHER 479
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                                                                                                                                                                                                                                                                                                                                                       -----CSFVAKTWTELLKHVRETH---KEEILCEVCRKTFKRK 229
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                                                                                                                                     RESULT 11
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Sequence 4, Application US/09262773
PATENT NO. 6225451
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 103;
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 727 amino acids
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REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994
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APPLICATION NUMBER: PC:
FILING DATE: 15-JUN-19:
CLASSIFICATION:
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NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 YHLSRHILTHTGEKPEVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parmelee, Stev REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
COMPUTER: IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 PPRP-----ALPRREICSEPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                               YALIQHQKSHKNEKRFKCDQCDYACRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLD 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG-----YVC-----QK 193
                                                                                                                                                                                                                                                                        MHFKRYHDPNFVPAAFVC··SKCGKTFTRRNTMARHADNCAGPDGVEGENGGETKKSKRG
                                                                                                                                                                                                                                                                                                                                                                                     DYLKQHMKTHAPER-----DVC--RCPRE-------GCGRTYTTVFNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                         GTMKMHILQKHTENVAKFHCPHCDTVIARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVSKLKRHIRSHTGERPFQCSL--CSYASRDTYKLKRHMRTHSGEKPYECYICHARFTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLLRNHLNTHTGTRPHKC--PDCDMAFVTSGELVRHRRYKH-THEKPFKCSM--CDYASV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPKPTKIKKKGVKKTFQCEL--CSYTCPRRSNLDRHMKSHTDERPHKCHL--CGRAFRTV 306
                                                                                                                                                                                                                                                                                                          SHILSFHEES----RPFVCEHAGCGKTFAMKQSLTRHA-VVHDPD------KKKMKL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                               G------KEEILCEVCRKTFKRK
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27.6%;
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Pred. No. 6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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264 479 229 419

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APPLICANT: Hess, Mark A.

TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE

TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1

FILE REFERENCE: Myriad 3

CURRENT APPLICATION NUMBER: US/09/262,773

CURRENT FILING DATE: 1999-03-04

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 640

TYPE: PAT

ORGANISM: human
US-09-262-773-4
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: MYY14d 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
LENGTH: 648
TYPE: PRT
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US-09-262-773-2
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                                                                           Query Match
Best Local S
Matches 95
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  372
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TNISQVNSFVNLRET---TPVHPLLGRHHDCSV--CGKSFTCNSHLVRHLRTHTGEKPYK 426
                                     SSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVRP-CRC--NECGKSFSRRDHLVRHQRT-HTGEKPFTC--PTCGKSFSRGYHLIRHQRT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV 300
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                                                                                95; Conser
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                                                                                Conservative
                                                                         15.6%; Score 313; DB 4; 31.6%; Pred. No. 2e-23; tive 44; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.6%; Score 313; DB 4; 31.6%; Pred. No. 1.9e-23;
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                                                                                                                 DB 4; Length 648;
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; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-486-099-117
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Query Match 15.6
Best Local Similarity 32.9
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117,
                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/486, FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFX: 66141 PENNIE
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                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                              STRANDEDNESS
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
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                                                                                                                                                                   LENGTH:
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Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
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                                                                                                               unknown
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                                                                                          protein
                 15.6%;
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   35;
                                                                                                                                                                                                                                                                                                     7872-031
Score 312.5; DB 3;
Pred. No. 1.4e-23;
15; Mismatches 101;
                                      Length 462;
   Indels
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                                                         ; MOLECULE TYPE: protein US-08-360-107A-127
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US-08-360-107A-127
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                                                                                                                                                               REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 127, Application US/08360107A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 20-DEC-1994 CLASSIFICATION: 435
                                                                                            TOPOLOGY:
                                                                                                            STRANDEDNESS
                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Matthews, Thomas J.
Wild, Carl T.
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15.6%;
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Score 312.5; DB 3; Pred. No. 1.4e-23;
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                   Length 462;
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; MOLECULE TYPE: US-08-484-223B-117
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US-08-484-223B-117
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Patent No. 6020459
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                                                                                                    TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.T.

ZIT: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
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                                                                                                                                                                                                                    NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: Patenti
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                                  TOPOLOGY:
                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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Langlois, Alphonse J.
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Query Match

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Search completed: February 10, 2003, 17:48:58 Job time: 28 secs
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                               290 MKQSLTRHAVVH 301
| | :| :|
389 RKNDLIKHQRIH 400
                                                                180 KRHAKAH---EGYVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEVCRKTFKRKDYLKQH 235
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	17	16	15	14	13	12	11	10	9	60	7	6	5	4	ω	2	1	Result No.
356.5	359	359	359	360.5	366	366.5	366.5	366.5	368.5	372	375	379	381	381	383.5	383.5	386	Score
17.8	17.9	17.9	17.9	18.0	18.2	18.3	18.3	18.3	18.4	18.5	18.7	18.9	19.0	19.0	19.1	19.1	19.2	Query Match Length DB
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US-09-864-761-36148	US-09-844-508-29	US-09-779-233-18	US-09-942-087A-30	US-09-925-301-1357	US-09-989-920-212	US-09-764-864-1065	US-09-974-298-118	US-09-864-761-42958	US-09-864-761-37152	US-09-864-761-37065	US-09-764-864-948	US-09-864-761-33653	US-09-828-648-2	US-09-976-165-10	US-09-764-864-1045	US-09-764-864-909	US-09-764-864-976	ID
Sequence 3/991, A Sequence 36148, A	Sequence 29, Appl	Sequence 18, Appl	Sequence 30, Appl	Sequence 1357, Ap	Sequence 212, App	Sequence 1065, Ap	Sequence 118, App	Sequence 42958, A	Sequence 37152, A	Sequence 37065, A	Sequence 948, App		Sequence 2, Appli	Sequence 10, Appl	Sequence 1045, Ap	Sequence 909, App	Sequence 976, App	Description

ALIGNMENTS

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RESULT 1

US-09-764-864-976

Sequence 976, Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PTZ23

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 976
LENGTH: 406
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
302
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                                                                                                                                                                                                                                                                                                                                       82 CSMNSHLIWPQKS----HTGEKPYEC--PECGKAFSEKSRLRKHQRTHTGEKPYKC--DG 133
                                     GCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKS-REKRSLASHLSGYIPPKRKQGQGLSL 341
                                                                                                                                                                                            EGCGKHFASPSKLKRHAKAHEG····YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEVC 222
                                                                                                                                                                                                                                               CDKAFSAKSGLRIH-QRTHTG-EKPFEC--HECGKSFNYKSILIVHQRTHTGEKPFECNE 189
                                                                                 GKAFGQKSQLRGHHRIHTGEKPY-KC--NHCGEAFSQKSNLRVHHRT-HTGEKPYQCEE- 301
                                                                                                        RKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHA 282
                                                                                                                                                                                                                                                                                             CDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQ 166
                                                                                                                                                                 -- CGKSFSHMSGLRNHRRTHTGERPYKCDE-CGKAFKLKSGLRKHHRTHTGEKPYKCNQC 246
-CGKTFRQKSNLRGHQRTHTGEKPYECNECGKAFSEKSVLRKH------
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342 CQNGESP-NC

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RESULT 3
US-09-764-864-1045
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US-09-764-864-909
US-09-764-864-1045
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APPLICANT: ROSEn et al.
APPLICANT: INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 909
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
                                                                        Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 1792 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1045
                                                                                                                                                                                                                                                                                Sequence 1045, Application US/09764864 Patent No. US20020132753A1
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                  ORGANISM: Homo
                                   LENGTH: 457
TYPE: PRT
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                sapiens
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                                                          Query Match
Best Local Similarity
"~+~hes 93; Conserve
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SEQ ID NO 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/565,538
PRIOR FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FUJIWARA, TSUTOMU APPLICANT: WATANABE, TAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/055,699 PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/976,165
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING
                                                                                                                                                                                                       LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Q-53599
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                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                     38 RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
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KSYVCI--ECGQAFIQKAHLIVHQRSHTGEKPYQC--HNCGKSFISKSQLDIHHRIHTGE 500
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30.8%;
                                                                                                    19.0%; Score 381; DB 1 32.9%; Pred. No. 5e-24;
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                                                                               43; Mismatches 119;
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Pred. No. 1.8e-24;
                                                                                                                       DB 10;
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Hanzel, David

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RESULT 6
US-09-864-761-33653
; Sequence 33653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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: SEQ ID NO 2
: LENGTH: 711
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-828-648-2
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US-09-828-648-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/828,648
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/246,331
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                             KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
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                                                                                                                                                                                                                                              KEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE--GCGRTYTTVFNLQSHILSFH 271
                                                                                                                                                                                                                                                                                             GEKPYKCSE--CGKAFTSKSQFKEHQRIHTGEKPYVCTE-CGKAFNGRSNFHKHQITHTR 611
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                                                                                                                                                                                                                     ERPFYCYKCGKAFVQKSELITHQRTHMGEK-----PYECLDCGKSFSKKPQLKVH-QRIH
                                                                                                                                                                                                                                                                                                                                                                    KPYEC--SDCGKTFTQKSHLNIH--QKIHTGERHHVCS--ECGKAFNQKSILSMHQRIHT
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Gendelman, Howard E.
University of Nebraska Medical Center
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Carlson, Kimberly
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Sharron G
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SEQ ID NO 33653
LENGTH: 525
TYPE: PRT
                                                                                         Query Match
Best Local
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2000-09-21
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: PCT/US01/00668
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OTHER INFORMATION:
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CSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATG 106
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                                                                                         Similarity
                                                                     Conservative
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NN: EXPRESSED IN HEART, SIGNAL = 1.8

NN: EXPRESSED IN HELA, SIGNAL = 1.9

NN: EXPRESSED IN HELA, SIGNAL = 1.9

NN: EXPRESSED IN BADULT LIVER, SIGNAL = 1.2

NN: EXPRESSED IN BATATA, SIGNAL = 0.96

NN: EXPRESSED IN BT474, SIGNAL = 2.6

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

NN: EXPRESSED IN HBL100, SIGNAL = 1.2

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
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                                                                Score 379; DB 10;
Pred. No. 5.1e-24;
9; Mismatches 123
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RESULT 8
US-09-864-761-37065
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; NAME/KEY: SITE
; LOCATION: (335)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-764-864-948
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Sequence 37065, Application US/09864761 Patent No. US20020048763A1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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SEQ ID NO 948
LENGTH: 338
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Best Local
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1792
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                                                                                                                                                                                                    QNVRPFVCTECGMEFSQIHHLKQHSLTHKGVKEF-KC--EVCGREFTLQANMKRHML-IH
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                                                                                                                                                               EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-KMKLKVKKSREKRSLASHL 325
                                                                                                                                                                                                                                        THKEEILCEVCRKTEKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVFNLOSHILSFH
                                                                                                                                                                                                                                                                                                                 NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG-----YVCQKGCSFVAKTWTELLKHVRE 211
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93; Conser
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Pred. No. 6.5e-24;
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OTHER INFORMATION: MAP TO AC005261.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

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PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PPLICATION NUMBER: US 09/632,366

PRIOR PPLICATION NUMBER: US 09/632,366

PRIOR PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR PILING DATE: 2000-10-04

PRIOR PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-9-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

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PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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                                 Query Match
Best Local
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-01-29
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                                     Similarity
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Chen, Wensheng
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30.2%;
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5;
                            Score 372; DB 10;
Pred. No. 2.1e-23;
Mismatches
                                                                      Length 551;
76;
Gaps
18
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US-09-864-761-37152

; Sequence 37152, Application

; Patent No. US20020048763A1
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PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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                                                                                 APPLICATION NUMBER: US
                                                                                                          FILING DATE:
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                                NUMBER: US
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 37152
LENGTH: 515
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.9

NN: EXPRESSED IN HELA, SIGNAL = 2.8

NN: EXPRESSED IN PLACENTA, SIGNAL = 2.3

NN: EXPRESSED IN HEART, SIGNAL = 2.3

NN: EXPRESSED IN HEART, SIGNAL = 2.7

NN: EXPRESSED IN HBL100, SIGNAL = 2.7

NN: EXPRESSED IN HBL100, SIGNAL = 2.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN BP4744, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67

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NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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                                                                                           KPYECKECGKGFSRVSNLIQHQKTHSSAKPFVCK----ECRKTFRYHYQLTEH-YRIHTG
                                                                                                                                                     EEILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEE 273
                                                                                                                                                                                                                   KPFECKE--CGKAFSLHTQLNHHKNIHTGEKPFKC-KECGKSFNRVSNLVQH-QSIHAGV
                                                                                                                                                                                                                                                                                 PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETHK--
                                                                                                                                                                                                                                                                                                                                                                                                            FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
                                                                                                                                                                                                                                                                                                                                               FECKE--CGKFFRRGSNLNQH--RSIHTGKKPFEC--KECGKAFRLHMHLIRHQKFHTGE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FECK--DCGKAFNRGSNLVQHQSIHTGEKPYEC--KECGKAFRLHLQLSQHEKTHTGEKP
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RESULT 12
US-09-764-864-1065
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Best Local S
Matches 94
                                                                                                           SOFTWARE: PatentIn
SEQ ID NO 1065
LENGTH: 547
                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                          Sequence 1065, Application Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PERL Program SEQ ID NO 118 LENGTH: 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/236,331
PRIOR FILING DATE: 2000-05-10
                                                                                                                                                          Prior application data removed - NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST
FILE REFERENCE: PA-0037 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 194
           NAME/KEY: SITE LOCATION: (289) OTHER INFORMATION:
                                                                            TYPE: PRT
ORGANISM: Homo
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NAME/KEY:
                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                              EHAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKTFKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVFNLOS---HILSFHEESRPFVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKVFSQNSYLAYHWRIHTGEK-AYKC--NECGK----VFGLNSSLAHHRKIHTGEKPFKC
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35.3%;
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Pred. No. 5.5e
36; Mismatches
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Best Local Simi
Matches 116;
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 212
LENGTH: 610
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 212, Application US/09989920 Patent No. US20020172957A1
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Best Local Similarity 29.9%;
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung
FILE REFERENCE: DEX-0291
CURRENT FILING DATE: 2001-11-21
CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                 70
                                                                                                                                                                                                    10 SYSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERP 69
                                                                                           YKCDV--CGKAYISRSSLKNHKGIHLGEKPYKCSY--CEKSFNYSSALEQH--KRIHTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRS-LASH 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPYDCNECGKSFGRSSHLIXXRHPTGEKPHKCNECGKSFCRLSHLIQH-QRTHSG-EKPY
                     KPFGC--DECGKAFRNNSGLKVHKRIHTGERPYKC--EECGKAYISLSSLINHKSVHPGE 272
                                                       KQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGY 189
                                                                                                                            FVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQ 129
                                                                                                                                                                  SYNSLLLQHRTIHTGE------RPYVCDV--CGKTFRNNAGLKVHRRLHTGEKP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYECNACGKS----FSRSSHLITHQKIHTGEKPYECNECWRSFGERSDLIKHQRTHTGEK 493
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                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                        18.2%; Score 366; DB 9; Length 610; 27.1%; Pred. No. 7.4e-23; Live 52; Mismatches 136; Indels 1
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; Pred. No. 5.9e+23;
47; Mismatches 116; Indels 81;
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1357
LENGTH: 580
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-09-925-301-1357
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
 470
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                                                                                                                                                                                                                     DCGRAFTVSSCLSQHM - - KIHVGEKPYEC - - KECGIAFTRSSQLTEHLKTHTAKDPFEC -
                                                                                                                                                                                                                                                        GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                            ECGKGFRYSAYLNIHMGTHTGDNPYEC--KECGKAFTRSCQLTQHRKTHTGEKPYKC--K 302
                                                                                                                                                                                                                                                                                                                              DCSANYSKAWKLDAHLCKHTGERPFYCDYEGCGKAFIRDYHLSRHILTHTGEKPFYCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CECGKSFN 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFAMKQSLTRHAVVHDPDK-----KKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSL
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-LECGKAFTHSSSLNNHMRTHSAKK 493
                                  HAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                      ECGKAFARSSRLSEHTRTHTGEKPF-ECVK--CGKAFAISSNLSGH-LRIHTGEKPFEC-
                                                                                                          VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE 280
                                                                                                                                               -KICGKSFRNSSCLSDHFRIHTGIKPYKC-KDCGKAFTQNSDLTKHAR-THSGERPYECK
                                                                                                                                                                                 QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETHKEE--ILCE
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APPLICANT: Lai, Albert

APPLICANT: Snowden, Andrew
APPLICANT: Tan, Siyuan
APPLICANT: Gregory, Philip
TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
FILE REFERENCE: 8325-0002.21 / S2-US5
CURRENT APPLICATION NUMBER: US/09/942,087A
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEO ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 30
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-942-087A-30
y Sequence 30, Application US/09942087A
patent No. US20020160940A1
GENERAL INFORMATION:
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Search completed: February 10, 2003, 17:49:31 Job time: 22 secs
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; OTHER INFORMATION: Description of Artificial Sequence:designed
; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-942-087A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.9%; Score 359; DB 9; Length 196; Best Local Similarity 34.3%; Pred. No. 7.2e-23; Matches 74; Conservative 26; Mismatches 80; Indels 36; Gaps
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                                                                                                                                                                                                                                       144 KKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWT 203
                                                                                                     164 -----EKKFACPECPKRFMRSDHLSRHIKTH 189
                                                                                                                                                  204 ELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTH 239
                                                                                                                                                                                                      119 GTTSNLRRHLRWHTGERPFMCTWSYCGKRFTRSSNLQRHKRTHTG---
                                                                                                                                                                                                                                                                                                            62 RTHTGEKKFACPE--CPKRFMRSDELSRHI-KTHQNKKDGGGSGKKKQHICHIQGCGKVY 118
                                                                                                                                                                                                                                                                                                                                                  92 LTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHEN------QQKQYICSFEDCKKTF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                             32 PRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGGGKAFIRDYHLSRHI 91
                                                                                                                                                                                                                                                                                                                                                                                                                    2 PIPGKKKQHICHIQGCGKVYGQSSDLQRHLRWHTGERPFWCTWSYCGKRFTRSSNLQRHK 61
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 10
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Pending_Patents_AA_Main:*

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14: //gqn2_6/ptodata/1/paa/US

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Gapop 10.0 , Gapext 0.5
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784.425 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2008 2008 2000 2000 2000 821 821	;
100.0 100.0 99.6 99.6 40.9 40.9	Query Match Length DB ID
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22 22 25 26	DB
365 22 US-09-831-426-2 365 22 US-09-831-426C-2 409 1 PCT-US00-2524B-5945 409 25 US-10-106-698-5955 184 1 PCT-US01-18569-2978 184 26 US-10-264-049-2978	ID
Sequence 2, Appli Sequence 2, Appli Sequence 5945, Ap Sequence 5955, Ap Sequence 2978, Ap Sequence 2978, Ap	Description

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Sequence 33849, A	Sequence 11, Appl	Sequence 16, Appl	equen	Sequence 3604, Ap	equen	Sequence 33156, A	Sequence 2341, Ap	Sequence 56, Appl	Φ	Sequence 49, Appl	16100,		16736,	Ð	e 20385,	54, App	6, Appl	e 14	Sequence 1833, Ap	32,	487	3577,	1609,	e 1394,	1389,		3644, 1	e 1355,	e 1355	Ce 32185		1961,	3929,	39706,	e 255,	æ	e 255,	pequence 1024, Ap

ALIGNMENTS

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Sequence 2, Application US/09831426

Sequence 2, Application US/09831426

GENERAL INFORMATION:
APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
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Sequence 2, Application US/09831426C
GENERAL INFORMATION:
APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIIA gene and cor
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NOS 10
SOFTWARE: Patentin Vers. 2.0
LENGTH: 365
TYPE: PRT
ORGANISM: Human
US-09-831-426C-2
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                                                                          HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA 360
                                                                                                                              PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV 300
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Sequence 5955, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer As
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/Z6524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5945
LENGTH: 409
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PCT-US00-26524B-5945
; Sequence 5945, Application PC/TUS0026524B
; GENERAL INFORMATION:
; APPLICANT: Birse et. al.
; TITLE OF INVENVION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005PCT
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Best Local Similarity
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                                                                                                                                                                                                                                                           Sequence 2978, Application PC/TUS0118569
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA133PCT
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Matches
                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2978
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PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5955
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LOCATION: (26)
OTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (123)
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.7e-163;
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US-10-264-049-2978
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                                                                                                                                                                                                                                              US-10-264-049-2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 2978
LENCTH: 184
TYPE: PRT
                                                                                                                                                                                                 Query Match
Best Local
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic acids, Proteins,
FILE REFERENCE: PA133P1
                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (123)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE LOCATION: (26)
OTHER_INFORMATION: Xaa
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 132
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                                                                                                                                     193 KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREG
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                                                                                                                   KRMSLCGKTWADLLXHVREPIKREXLCGVCRKTFNAKDYLKQPMKTHAPERDVCRCPREG
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                                                          CGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLPRHAVVHDPXKKKMKLKV
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Pred. No. 3.9e-62;
Pred. No. 3.9e-62;
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Pred. No. 3.9e-62;
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RESULT 7 US-09-760-466-1024 ; Sequence 1024, Application US/09760466

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US-10-212-083-1024
; Sequence 1024, Application US/10212083
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 258 ; SOPTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 255 ; LENGTH: 106 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-760-494-255
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LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-466-1024
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US-09-760-494-255
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Best Local :
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                                            TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTES9CIN
CURRENT APPLICATION NUMBER: US/10/212,083
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 09/760,466
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
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CURRENT FILING DATE: 2001-01-16
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/760,494
CURRENT FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-01-31
APPLICATION NUMBER: 60/180,628
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ilarity 100.0%; Pred. No. 1.3e-39;
Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2000-08-14
PRIOR PPLICATION NUMBER: 60/220,963
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-26
PRIOR PPLICATION NUMBER: 60/217,496
PRIOR PPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
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Best Local Similarity
Matches 106; Conserv
                                                                                   SOFTWARE: PatentIn SEQ ID NO 255
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GENERAL INFORMATION:
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SEQ ID NO 1024
LENGTH: 106
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CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/760,494
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
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PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-14
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ORGANISM: Homo sapiens
                                                     LENGTH: 106
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14
                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/218,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-02-04
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                                                                                                                                                                      See File Wrapper or PALM
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 39706
LENGTH: 95
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PCT-US01-08631-39706
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                                                      CURRENT APPLICATION NUMBER: PCT/US01/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR EILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR PPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR APPLICATION NUMBER: 09/663,561
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PCT-US01-04098A-3929
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-049
                                                                                                                                                                                                                                                                                                    Sequence 3929, Application PC/TUS0104098A GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-029
                                          PRIOR
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                       PRIOR
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OTHER INFORMATION: C2H2-TYPE ZINC FINGER SIGNATURE domain identified by eMATRIX,
OTHER INFORMATION: accession number PR00048A, p-value-4.240e-09, raw score of 10.52
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                  FILING DATE: 2000-09-15
APPLICATION NUMBER: 09/654,936
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  DATE:
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Pred. No. 1.3e-39;
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Pred. No. 8.6e-31;
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                                                                                                                                  CURRENT APPLICATION NUMBER: PCT/US01/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
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SEQ ID NO 3929
LENGTH: 927
TYPE: PRT
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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GENERAL INFORMATION:
APPLICANT: Hyseq, I
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                                                      PRIOR FILING DATE:
                                                                         PRIOR APPLICATION NUMBER: 09/620,325
                                                                                              PRIOR APPLICATION NUMBER: 09/654,936 PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 21272-029
                                     PRIOR
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                APPLICATION NUMBER: 09/598,075 FILING DATE: 2000-06-20
APPLICATION
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NUMBER: 09/560,875
                                                        2000-07-19
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Pred. No. '
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cches 115;
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458 243 399 285 102

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PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEO ID NOS: 3960

SOFTWARE: CUSTOM
SEO ID NO 1961
LENGTH: 869

TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-04098A-1961
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                                                             PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR PPLICATION NUMBER: 09/663,561
PRIOR PRILING DATE: 2000-09-15
PRIOR PPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER: 09/598,075
PRIOR PRIOR PRIOR NUMBER: 09/598,075
PRIOR PRILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR PRILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US01-04098A-1676; Sequence 1676, Application PC/TUS0104098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hyseq, I
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Nucleic Acids and FILE REFERENCE: 21272-029
SOFTWARE: Custom
                                                NUMBER OF SEQ ID NOS: 3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 DK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 DVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 21.0%; Score 421; DB 1; Local Similarity 32.0%; Pred. No. 8.6e-27; Des 116; Conservative 41; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVC------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV------AKTWT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIHTGERPNTC--SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVVPANEPSLRELVQG------RPAGAEKPYICN--ECGKSFSQWSKLLRHQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PY-KCPE--CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEKPYECLECGKSFGHSSTLIKHQR-THLREDPFKCPVCGKTFTLSATLLRHQRTHTGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPER 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTGEEPYKCTECEIAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTGEKPYKCPE--CGKRFGQNHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AATGCDQKENTKSNLKKHEERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides
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US-10-029-386-32185; Sequence 32185, Application US/10029386; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine SEQ ID NO 32185
LENGTH: 803
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1676
LENGTH: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 80
TYPE: PRT
OTHER INFORMATION: MAP TO Z99130.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7

OTHER INFORMATION: SWISSPROT HIT: P98169, EVALUE 0.00e+00
                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 ELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 KHSMKTHM----VKRHKVGQDL 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 VHLLTHSSSQGQRPFKCPLGGCGWTFTTSYKLKRHLQSHDKLRPFGCPAEGCGKSFTTVY 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 DLLLAEPAEPAPAPAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPEAQCGQTFAKKHQLK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 DAFIAAGESSAPTP------PRPALPRR-----FICSFPDCSANYSKAWKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH--DPDKKKMKLKV----KKSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLKKHF-----ERKHENQOKQYICSFEDCKKTFKKHQQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHLCKHT---GERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRSLASHLSGYIPPKRKQGQGL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSRCPISSCNKLFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLLRH------KRK-----HDDDRRF-MCPVEGCGKSFTRAEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLKAHMKGHEQENSFKCEVCEESFPTQAKLSAHQRSHFEPERPYQCAFSGCKKTFITVSA 409
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 417.5; DB 1
Pred. No. 1.6e-26;
                                                                                                                                                                                                                                                                                                                                                          vers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 803;
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Query Match Best Local Similarity

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Score 417.5; DB 24; Length 803; Pred. No. 1.6e-26; 7; Mismatches 131; Indels 93;

Gaps

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Sear	ДĎ	Qy	DЬ	Qy	В	Qy	Ф	Qγ	В	Qy	Ф	Qy	ф	VΩ
cor cor	561	318	502	264	470	204	410	149	350	116	290	59	230	18
Search completed: February 10, 2003, 17:55:41	KHSMKTHMVKRHKVGQDL 578	KRSLASHLSGYIPPKRKQGQGL 339	KGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSRCPISSCNKLETS 560	- =	KLLRH	VRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCF	LFSHNRAHFREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCDFDGCGWNFTSMS 469	LKIHQCQHTNE-PLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ-KGCSFVAKTWT 203	NLKAHMKGHEQENSFKCEVCEESFPTQAKLSAHQRSHFEPERPYQCAFSGCKKTFITVSA 409	NLKKHFERKHENQQKQYICSFEDCKKTFKKHQQ 148	290 VHLLTHSSSQGQRPFKCPLGGCGWTFTTSYKLKRHLQSHDKLRPFGCPAEGCGKSFTTVY 349	CDYEGCGKAFIRDYHI	DLLLAEPAEPAPAPAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPEAQCGQTFAKKHQLK 289	DAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLD 58

Search completed: February 10, 2003, 17:55:41 Job time : $304 \ \text{secs}$

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Minimum DB
Maximum DB
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No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1992

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Match Length
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Gapop 10.0 ,
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2008
1 MDPPAVVAESVSSLTIADAF......ESPNCVEDKMLSTVAVLTLG
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Oy 363 TLG 365 Db 361 TLG 363	Qy 303 PDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLC	Qy 243 RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQS	Qy 183 AKAHEGYVCQKGCSEVAKTWTELLKHVRETHKEEILCEVCRKTEKRKDYLKQHMKTHAP	QY 123 RKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRH	Qy 63 KHTGERPFVCDYEGGGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHF 	Qy 3 PPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLC	Query Match 99.2%; Score 1992; DB Best Local Similarity 99.7%; Pred. No. 1.2e-1 Matches 362; Conservative 0; Mismatches	A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-53 CRES> A;Cross-references: EMBL:U20272; NID:9644870; PIDN: C;Superfamily: transcription factor IIIA	A; Pittle: Cloning and expression analysis of a human A; Reference number: 138937; MUID:95347600; PMID:76: A; Accession: 138937	ion: I38937 P.D.; Nagle, J.W.; Canning, R.D.; Ozato,	RESULT 1 I38937 DNA/RNA-binding protein - human (fragment) C;Species: Homo sapiens (man) C;Cate: 29-May-1998 #sequence_revision 29-May-1998	ALIGNMENTS	31 371 18.5 1191 2 335305 32 368.5 18.4 654 2 A57785 33 368.5 18.4 673 2 355335 34 368 18.3 435 2 \$00833 35 367.5 18.3 576 2 A48157 36 367 18.3 576 2 A48157 37 366.5 18.3 428 2 \$51037 38 365.5 18.2 399 2 \$47071 39 365.5 18.2 399 2 \$47071 40 364.5 18.2 580 2 A37107 40 364.5 18.2 580 2 A37898 41 363.5 18.1 393 2 JN0533 42 363.5 18.1 469 2 138600 43 363.5 18.1 553 2 \$22954 44 362.5 18.1 553 2 \$22954	0 371 18.5 728 2
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transcription factor IIIA - African clawed frog
N;Alternate names: factor A; TFIIIA
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 21-Jul-2000
C;Accession: A90857; A24961; S21776; A05529; A91007; S40784; S40785
R;Ginsberg, A.M.; King, B.O.; Roeder, R.G.
Cell 39, 479-489, 1984
A;Title: Xenopus 5S gene transcription factor, TFIIIA: characterization of a cDNA clone
A;Reference number: A90857; MUID:85074456; PMID:6210149
A;Accession: A90857
A;Title: Repetitive zinc-binding domains in A;Reference number: A91007; MUID:85284956; PA;Contents: annotation R;Smith, J.F.; Hawkins, J.; Leonard, R.E.; H
                                                                         A; Molecule type: mRNA
A; Residues: 1-344 <GIN>
A; Cross-references: GB:KO2938; NID:g214818;
R; Miller, J; McLachlan, A.D.; Klug, A.
EMBO J. 4, 1609-1614, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: G07520
A;Accession: G01496
A;Status: preliminary; translated from
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N;Alternate names: TFIIIA
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G01496
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A;Map position: 13q12.3-13q13.1
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A; Residues: 1-338 <BEC>
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RESULT JC1441

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A;Introns: 40/3; 74/2; 106/3; 136/2; 161/1; 190/1; 266/3; 284/3 (Superiamily: transcription factor IIIA C:Keywords: DNA binding: duplication; nucleus; tandem repeat; tref.5-37/Region: zinc finger CCHH motif F:45-67/Region: zinc finger CCHH motif F:75-98/Region: zinc finger CCHH motif F:107-129/Region: zinc finger CCHH motif F:137-159/Region: zinc finger CCHH motif F:137-159/Region: zinc finger CCHH motif F:144-148/Region: zinc finger CCHH motif F:154-214/Region: zinc finger CCHH motif F:154-214/Region: zinc finger CCHH motif F:154-214/Region: zinc finger CCHH motif F:233-246/Region: zinc finger CCHH motif F:254-276/Region: zinc finger CCHH motif
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A; Molecule type: DNA
A; Residues: 1-296, 'C', 298-312, 'I', 314-333, 'D', 335-342, 'L', 344 <TSO>
A; Residues: 1-296, 'C', 298-312, 'I'; BIDN:CAB51745-1; PID:g5579716
A; Cross-references: EMBL:X03681; NID:g65111; PIDN:CAB51745-1; PID:g5579716
R; Liao, X.; Clemens, K.R.; Tennant, L.; Wright, P.E.; Gottesfeld, J.M.
J. Mol. Biol. 223, 857-871, 1992
A; Title: Specific interaction of the first three zinc fingers of TFIIIA with
A; Reference number: S21776; MUID:92167265; PMID:1538401
A; Accession: S21776
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R;Residues: 1-101 <LIA>
R;Residues: 1-101 <LIA
Nucleic Acids Res. 19, 6197-6203, 1991
Nucleic Acids Res. 19, 6197-6203, 1991
A;Title: High yield purification of active transcription factor IIIA expressed A;Reference number: $40784; MUID:92066468; PMID:1956778
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 14, 2187-2200, 1986
A; Title: Structure of the gene for Xenopus
A; Reference number: A24961; MUID:86176722;
A; Accession: A24961
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A;Title: Structural elements in the N-terminal half of transcription factor IIIA A;Feference number: S40785; MUID:92107675; PMID:1762917
A;Contents: annotation; site-directed mutagenesis
R;Tso, J.Y.; Van Den Berg, D.J.; Korn, L.J.
Nucleic Acids Res. 14, 2187-2200, 1986
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                                                                                                                                             EESRPEVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGY1PP 331
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KSKE-KNASVSGTEKTDSLVKNKPSGT
                                                     KRKQGQGLSLCQNGESPNCVEDKMLST 358
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A;Cross-references: GB:#32472; NID:g214150; PIDN:AAA49713.1; PID:g214151
R;Gaskins, C.J.; Hanas, J.S.
Nucleic Acids Res. 18, 2117-2123, 1990
A;Title: Sequence variation in transcription factor IIIA.
A;Reference number: S09653; MUID:90245658; PMID:2110661
A;Recession: S09653; MUID:90245658; PMID:2110661
A;Accession: S09653; MUID:90245658; PMID:2110661
A;Accession: S09653
A;Molecule type: mRNA
A;Residues: 1-221, 'C', 223-234, 'E', 236-291, 'R', 293-309, 'S', 311-313, 'A', 315-318, 'G', 320-33
A;Residues: 1-221, 'C', 223-234, 'E', 236-291, 'R', 293-309, 'S', 311-313, 'A', 315-318, 'G', 320-33
A;Cross-references: EMBL:X17695; NID:g64474; PIDN:CAA35689.1; PID:g64475
C;Superfamily: transcription factor IIIA
C;Keywords: DNA binding: nucleus; transcription factor; zinc finger
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B34895
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;Species: Rana pipiens (northern leopard frog)
C:Date: 30/Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-
C:Accession: JC1441
R:Gaskins, C.J.; Smith, J.F.; Ogilvie, M.K.; Hanas, J.S.
Gene 120, 197-206, 1992
A:Title: Comparison of the sequence and structure of transcription
A:Reference number: JC1441; MUID:93013035; PMID:1398134
                                                                                                                                                                                                                                                           transcription factor IIIA - Kenyan clawed frog

C;Species: Xenopus borealis (Kenyan clawed frog)

C;Date: 20-Jul-1990 #sequence_revision 21-Oct-1992 #text_change

C;Accession: B34995; S09653

R;Joho, K.E.; Darby, M.K.; Crawford, E.T.; Brown, D.D.

Cell 61, 293-300, 1990

A;Title: A finger protein structurally similar to TFIIIA that bi

A;Reference number: A34895; MUID:90235278; PMID:2331751

A;Accession: B34895
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C;Superfamily: transcript
C;Keywords: DNA binding;
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A; Residues: 1-335 <GAS>
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C; Keywords: DNA binding; duplication; nucleus; transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Comparison of the sequence and structure of transcription A; Reference number: JC1441; MUID:93013035; PMID:1398134 A; Accession: JC1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor IIIA - American toad
C:Species: Bufo americanus (American toad)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C:Accession: JC1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.1 Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQK--GCSFVAKTWTELLKHVRE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 189; Conserv
                                                                                                                                                                                                                                              CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKG--CSFVAKTWTELLKHVRE
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                                                                                                                                                             THKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFH
                                                                                                                                                                                                                     YIHTNQQPFKCSHEGCDKCYASPSRLKRHEKTHAGYPCRKDSTCPFVGKTWSDYMKHAAE
                                                                                                                                                                                                                                                                                                                                                                              PALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHQEPVMCDECKRTFKHKDYLRNHKKTHKKERTVYRCPRDGCERSYTTAFNLQSHMQSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALPRREICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILT
                ---PKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL
                                                                                                EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIP-
                                                                                                                                        LH-SEVTCSICNRTFKRKSFLKEHKKIHREERIVYRCPRENCDRTYTTKFNLKSHILTFH
                                                                                                                                                                                                                                                                                                   HTGEKPCKCETENCNLAFTTASNMRLHFKRAHSSPAQVYVCYFADCGQQFRKHNQLKIHQ
                                                                                                                                                                                                                                                                                                                                           HTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ
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                                                          ENLRPFVCEHEGCGKTFAMKQSLDRHFNTHDPEKKKM---VKPPRPVRSLASRLSGYKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.9%;
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6; Mismatches
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Pred. No. 3.
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ches 80;
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RESULT 7
C34895
SS RNA-binding protein p43 - African clawed frog
SS RNA-binding protein p43 - African clawed frog)
C:Species: Xenopus laevis (African clawed frog)
C:Species: 20-Jul-1990 #sequence_revision 21-Oct-1992 #text_change 21-Aug-1998
C:Accession: C34895
R:Joho, K.E.; Darby, M.K.; Crawford, E.T.; Brown, D.D.
Cell 61, 293-300, 1990
A;Tille: A finger protein structurally similar to TFIIIA that binds exclusively
A;Reference number: A34895; MUID:90235278; PMID:2331751
A;Accession: C34895
A;Status: preliminary; nucleic acid sequence not shown
A;Residues: 1-365 < JOH>
C:Superfamily: transcription factor IIIA
C:Superfamily: transcription factor IIIA
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                  A; Title: A finger protein structurally similar to TFIIIA A; Reference number: A34895; MUID:90235278; PMID:2331751 A; Accession: A34895
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
A34895
SS RNA-binding protein p43 - Kenyan clawed frog
C;Species: Xenopus borealis (Kenyan clawed frog)
C;Date: 20-Jul-1990 #sequence_revision 21-Oct-19
C;Accession: A34895
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A;ResIdues: 1-365 <JOH>
C:Superfamily: transcription factor IIIA
C;Keywords: DNA binding; zinc finger
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Best Local :
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MKRHLTLKKHSCPTAGCKMTFSTKKSLSRHKLYKH-GDAVPLKCSVPGCKRSFRKKRALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVCDVPGCSWKSSSVAKLVAHQKRHRGYRCSYEGCQTVSPTWTALQTHVKK-HPLELQCA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPTAGCKMTFSTKKSLSRHKLYKH-GEAVPLKCFVPGCKRSFRKKRALRRHLSVHSNEPL 135
                                                                                                                                 PPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106;
                                                   ILTHTGEKPFVCAATGCDOKFNTKSNLKKHFERKHENOOKOYICSFEDCKKTFKKHQQLK 150
                                                                                            PTEPSKSQVFRCPAAGCKAVYRKEGKLRDHMAGHSEQKLWKCGKKDCGKMFARKRQIQKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACKKPFKKASALRRHKATHAKKPLQLPCPRQDCDKTFSSVFNLTHHVRNVHLCLQTHRCP 254
                                                                                                                                                                          Similarity 37.4
)8; Conservative
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38.1%;
                                                                                                                                                                       27.6%; Score 553.5; DB 2; 37.4%; Pred. No. 1.3e-34; tive 48; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                     not shown
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            finger protein (clone xlcGF57-1) - African clawed frog (fragment) C:Species: Xenopus laevis (African clawed frog) C:Cpate: 28-Feb-1990 *sequence_revision 28-Feb-1990 *text_change 3 C:Accession: S06578 R:Nietfald, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, J. Mol. Biol. 208, 639-659, 1989 A:Title: Second-order repeats in Xenopus laevis finger proteins.
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#text_change 31-Dec-1993

Koester, M.;

Poeting,

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zinc-finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Accession: T37676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
A;Introns: 50/3
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
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A; Accession: T37676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: AL132675; PA; Experimental source: strain 972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-374 <MCD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETHKEEILCEVCRKTFKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHVSEHSNEPLSVCDVPGCGWKSTSAAKLAAHHRRHGGYRCSYEDCQTVSPTWTALQTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ-KGCSFVAKTWTELLKHV 209
                                                                                                                                                                                                                                                                                                                                                                                                    FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH-QCQHTN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KK-HPLELQCAACKKPFKKASALRRHKATHAKNPLQLPCPRQDCDKIFSTVFNLTHHLRK
HDQKEKELSSNLVSDVAKK-IINEVTGH
                                                                                                                                                                                                                                                                                 LLPYPCTYQDCELRFATKQKLQNHVNRAHEKIISYSCPHESCVGHEGF--EKWSQLQNHI
                                                                                                                                                                                                                                                                                                         FSCHYDGCDAQFYTQQHLERHIE--VHRKPKPYACTWEGCDECFSKHQQLRSHISACHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHCPYEECGKKYSRPSLLEQHLRTHSNERPFVCDYTGCSKAFYRKSHLK1HKRCHTNVKP
                                             HDPDKKKMKLKVKKSREKRSLASHLSGY 328
                                                                                                                                                                                      REAHVPS--CSICGRQFKTAAHLRHHVVLHQTTLEERKTYHCPMEGCKKSFTRSSALKKH
                                                                                                                                                                                                                                 RETHKEEILCEVCRKTFKRKDYLKQHMKTH---APERDVCRCPREGCGRTYTTVFNLQSH 266
                                                                                             ISVIHEGNMAFHCD--SCGTKFGYKHMLQRHLERGTCKKAHKPYINECGIKHDGIEGVAI
                                                                                                                                           ILSFHEESRPFVCEHAGCGKTFAMKQSLTRH-----
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109; Conserv
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33.2%; pred. No. 3.1e-30;
tive 48; Mismatches 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00066;
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R:Abrink, M.; Aveskogh, M.; Hellman, L.

DNA Cell Biol. 14, 125-136, 1995

A:Title: Isolation of cDNA clones for 42 different Kruppel-related A; Reference number: 137566; MUID:95169271; PMID:7865130

A:Accession: 137570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zinc finger protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
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A; Residues: 1-336 <NIE>
C; Keywords: DNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S05632; A; Accession: S06578 A; Status: not compared with
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A; Residues: 1-693 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                          Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSECGKKYSQIVNLASHM 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPFTCTECGKAFTLKGSLVGHMKIHTGEKPF-SCTQ--CGKNFTQKNSLLCH-LTMHTGE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPFTCTE--CGKNFAQKTNLLCHLKIHTGEKPFTCTECGDKFAKK--NNLLRHLKIHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSC--TECGKHFAHKGHLVSHM--KTHTGEKPFTCT--ECGKHFAQKGHLVSHMKTHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                  DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FICT -- ECGKGFSQKGILQTHMKTHTGEKPFTC--TECGKNFAQITTLLRHLTIHTGEKP
AKTWTELLKH----VRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG | :: : : : : : : : | | | | | |
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                                                                               QEGCGKHFASPSKLKRHAKAHEG --- YVCQ --- KG ----
                                                                                                                                             GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                             ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFTCTECGKGFALKGNLVLHTKIHTGEKPFSCTQCGKNFAQKNSLLRHLKIHTREKPFT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPFVCEHAG-----
                                               -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
                                                                                                               -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC- 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zinc finger
                                                                                                                                                                                                                                          20.2%; Score 406; DB 2; Length 693; 30.9%; Pred. No. 3.9e-23; tive 42; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.4%; Score 409; DB 2; 34.0%; Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                            74;
                                                                               -CSFV 198
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                254
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             C; Accession: 138618
R; Tonmerup, N.: Vissing, H.
Genomics 27, 259-264, 1995
A; Title: Isolation and fine m
A; Reference number: A57785; M
A; Accession: 138618
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A54661
                                                                                                                                                            RESULT 13
138618
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                                                                                                          zinc finger protein ZNF143 - human
C:Species: Homo sapiens (man)
C:Date: 23-Feb-1996 #sequence_revision
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A; Residues: 1-542 <FRA>
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                         ----EHAG-----
                              mapping of 16 novel MUID:96044430; PMID
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                                                                                                                                                                                                                             537
                                                                                                                                                                                                                                                           333
                                                                                                            23-Feb-1996 #text_change
                            novel human z
PMID:7557990
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zinc finger protein ZNF41 - human (Iragment)
(;Speckes: Homo sapiens (man)
(;Date: 02-Jun-1995 *sequence_revision 02-Jun-1995 *text_change 01-Dec-
(;Accession: A54661; I54227
(;Accession: A54661; I54227
N: Rocchi, M.; Marino, M.; Grimaldi, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:125865; OMIM:314995
A;Map position: Xp11.3-Xp11.23
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Isolation and expression analysis of a human zinc finger gene (ZNF41) locate A;Reference number: A54661; MUID:91244317; PMID:2037297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Franze, A.; Archidiacono, N.; Rocchi, M.; Marino, Genomics 9, 728-736, 1991
                                                                                                                                                                                      217 ILCEVCRKTFKRKDYLKOHMKTHAPER-DVCRCPREGCGRTYTTVFNLOSHILSFHEESR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                           102 CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKSFRMKIHYQVHLVVHTGEKPYKCEVCGKAFRQSSYLKIHLKAHSVQKPF-KC--EECG 457
                                                                                                                          YECSDCGKCFTKKSQLRVHQKIHTGEKPNIC----AECGKAFTDRSNLITH-QKIHTREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CS--DCGKSFTKKSQLHVHQRIHTGEKPYIC--TECGKVFTHRTNLTTHQKTHTGEKPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQASHLLTHQRVHSGEK---PFKCEECGKSFSRSAHLQAH
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PYECGDCGKTFTWKSRLNIHQKSHTGERHYECSKCGKAFIQKATLSMHQ1IHTGKKPYAC
                                                                                                                                                                                                                                                                                                                 FKCTOEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE
                                                                                                                                                                                                                                                                                                                                                                                CAE--CGKAFTDQSNLIKH--QKTHTGEKPYKCN--GCGKAFIWKSRLKIHQKSHIGERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGY
                                                                                                                                                                                                                                                     YEC--KDCGKAFIQKSTLSVHQRIHTGEKPYVCPECGKAFIQK--SHFIAHHRIHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:M92443; NID:g340443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 404; DB 2; 1
Pred. No. 4.3e-23;
6; Mismatches 121;
                                                           CGKTFAMKQSLTRHAVVHDPDKKKMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAA61312.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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zinc

finger-encoding

CDNAS

iden

05-Nov-1999

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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues; 129-491, 'SD', 494-581 <NIE>
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
C;Keywords: RNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X70680; NID:g453465; PID:g453466
R;Klocke, B.; Koester, M.; Hille, S.; Bouwmeester, T.; Boehm, S.;
Blochim. Blophys. Acta 1217, 81-89, 1994
A;Title: The FAR domain defines a new Xenopus laevis zinc finger
A;Reference number: S41058; MUID:94114576; PMID:7506934
A;Accession: S65027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                finger protein XFO 6 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
C;Caccession: S6508B; S65027; S06544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S65088
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A; Residues: 1-626 <RES>
A; Ccross-references: EMBL:U09850;
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Second-order repeats in Xenopus laevis finger proteins A;Reference number: S05632; MUID:90040698; PMID:2509712 A;Accession: S06544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X70680
R;Nletfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester,
J. Mol. Biol. 208, 639-659, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-28; 30-99 < KLW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S65084
A; Accession: S65088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-591 < KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data
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Best Local S
Matches 79
                                                                                                                                                                                                                      Query Match
Best Local Similarity
311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 KAFRCEYDGCGKLYTTAHHLKVHERSHTGDRPYQCEHAGCGKAFATGYGLKSHVRTHTGE 282
                                                                                                                                                     46
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         ECGKSFTEKSILQKH-QRTHTG-EKPFTCT--ECGKSYSAMSTLECHRRTHTGEKPFTCT
                                    GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERPYYCTEPGCGRAFASATNYKNHVRIHTGEKPYVCTVPGCDKRFTEYSSLYKHHVVHT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
                                                                                                                               DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQ-KGCSFVAKTWTELLK-HVRET 212
                                                                                                       ECGKEFTSKYYLNVHKRLHTGEKPFTCTQ--CGKCFSDKSALKYHHKTHTGEKPFAC--T 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKEEILCEVCRKTFKRKDYLKQHMKT 238
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79; Conserv
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                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                              19.8%; Score 397.5; DB 2; 31.4%; Pred. No. 1.5e-22; tive 40; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library, January 1993
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              366
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Nucleic Acids Res. 19, 2921-2928, 1991
A;Title: A gene encoding 22 highly related
A;Reference number: S26823; MUID:91279444;
A;Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Thiesen, H.J.

New Biol. 2, 363-374, 1990

A:Reference number: 137949; MUID:91145339; PMID:2288909

A:Accession: 137967

A:Accession: 137967
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 19p13.1-19p12
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 476-531 <THI>
A; Cross-references: EMBL: X52358;
C; Genetics:
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A;Molecule type: mRNA
A;Residues: 1-803 <LOV>
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N;Alternate names: zinc finger protein kox27
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S26823; I37967; S10416
R;Lovering, R.; Trowsdale, J.
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A;Cross-references: GDB:128653
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Best Local S
Matches 107
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621
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CGKAFNQFSTLTKHKIIHTEEKPYKCEECGKAFKWSSTLTKHKIIHTGEK---PYKCEEC
                                                                          CGKAFTQSSNLTTHKKIHTGEK-FYKC--EECGKAFTQSSNLTTH-KKIHTGGKPYKCEE 620
                                                                                                                                                                         QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEV
                                                                                                                                                                                                                                                                     GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                             ECGKAFKWSSKLTEHKLTHTGEKPYKC -- EECGKAFNWPSTLTKHNRIHTGEKPYKCEV - 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SREKRSLASHLSGYIPPKRKQGQGLSLCQNGESP-----NCVEDK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG
                                                                                                            CRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEH 281
                                                                                                                                                                                                                                 -CGKAFNOFSNLTTH--KRIHTAEKPYKC--EECGKAFSRSSNLTKHKKIHIEKKPYKC-
                                                                                                                                                      -EECGKAFKWSSKLTEHKITHTGEKPYKCEE-CGKAFNHFSILTKHKRIHTGEKPYKCEE 564
                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Score 394.5; DB 2;
Pred. No. 3.4e-22;
4; Mismatches 133;
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                                  CGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKS 315
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PMID:1711675
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  677
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_21:*

1. sp_archea:*
2. sp_bacteria:*
3. sp_fungi:*
4. sp_human:*
5. sp_invertebrate
6. sp_mammal:*
7. sp_mbc:*
8. sp_organelle:*
9. sp_phage:*
10. sp_plant:*
11. sp_vordent:*
12. sp_virus:*
13. sp_vertebrate:
14. sp_unclassifit
15. sp_rvirus:*
16. sp_bacteriap:*
17. sp_archeap:*
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2008
1 MDPPAVVAESVSSLTIADAF.....ESPNCVEDKMLSTVAVLTLG 365
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
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sp_rvirus:*
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sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15 16	10 12 13	9876	15 & 4 Z	Result No.
405 404	406.5 406.5 5	496 425 416.5 414	1583.5 1582.5 1498 946.5 551.5	Score
			78.9 78.8 74.6 47.1	% Query Match
411 847 531	403 559 587 700	374 927 703 411	387 336 368	
444	2115	11 13	51111	BIG
P70046 Q9H559 Q9H176	Q9VXB4 Q91WM0 Q9Z2X6 Q96IR4	Q9UTL5 Q9UEG4 Q9R161 P70043	Q9CSH8 Q8VHT7 Q8VHT8 Q9CSW1 Q9CSW1	ID
970046 xenopus lae Q9h559 homo sapien Q9h176 homo sapien	O9vxb4 drosophila O91vm0 mus musculu O92zx6 mus musculu O96ir4 homo sapien	O9utl5 schizosacch O9ueg4 homo sapien O9r161 mus musculu P70043 xenopus lae	Q9csh8 mus musculu Q8vht7 mus musculu Q8vht8 rattus norv Q9csw1 mus musculu Q9w7d7 oryzias lat	Description

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Q96Jw6 homo sapien	Q9by31 homo sapien	xenc	homo	homo	Q96nh0 homo sapien	Q9xsrl canis famil	Q62886 rattus norv	ratt	homo	homo	Q62512 mus musculu	mus	0 mus	homo	Q96ir2 homo sapien	Q96qh6 homo sapien	homo	homo	Q9nr94 homo sapien		_	Q8wuk9 homo sapien	Q09046 xenopus lae	O61361 drosophila	O61360 drosophila	Q99j65 mus musculu	O61362 drosophila	Q9vkfl drosophila

ALIGNMENTS

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Nature 409:685-690(2001). EMBL; AK012797; BAB28476.1; HSSP; P03001; ITF3.	<pre>Hayashizaki Y.; "Functional annotation of a full-lengt</pre>	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts	A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	Control I M Ctantl C C C C C C C C C C C C C C C C C C C	•	Kadota K., Matsuda H.A., Ashburner M., Batai	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda						NCBI_TaxID=10090;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;			GTF3A OR 2010015D03RIK	2010015D03Rik protein (Fragment)	of-Jun-2001 (IIEMBLiel. 17, Last sequence update) 1 01-Jun-2002 (TremBLrel. 21, Last annotation update)	01-JUN-2001 (TrEMBLrel. 17, Created)	Q9CSH8;		RESULT 1 Q9CSH8

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SEQUENCE
                                            PROSITE;
PROSITE;
NON_TER
                                                                                                                                                             SEQUENCE FROM N.A.

MEDILINE=21673987; PubMed=11814676;
Hanas J.S., Hocker J.R., Cheng Y.-G., Lerner M.R., Brac
Lightfoot S.A., Hanas R.J., Madhusudhan K.T., Moreland
"cDNA cloning, DNA binding, and evolution of mammalian
factor IIIA.";
Gene 282:43-52(2002).
EMBL; AF391799; AAL69686.1; -
MGD; MGI:1918846; Gtf3a.
InterPro: IPR000822; Znf_CCH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBVHT7 PRELIMINARY; PRT; 400 AA. QBVHT7; 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transcription factor IIIA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00028; ZINC_FINGER_C2H2_1; PS0517E; PS50157; ZINC_FINGER_C2H2_2; DNA-binding; Zinc-finger.

NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00096; zf-C2H2; SMART; SM00355; ZnF_C2H2
                                                                                                              Pfam; PF00096; zf-C2H2; 9. SMART; SM00355; ZnF_C2H2; 9.
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                                                                  PS00028;
PS50157;
                        400 AA;
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ZnF_C2H2; 9.
                                                                  ZINC_FINGER_C2H2_1;
ZINC_FINGER_C2H2_2;
                      45417
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77.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1583.5; DB 11;
Pred. No. 8.7e-139;
""-matches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                        EDFFFA8D8D26EAFD CRC64;
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Best Local S
Matches 283
                                                                                                                                     Query Match
Best Local S
Matches 265
                                                                                                                                                                                                                                                                                                                               Pfam; PF00096; Zf-C2H2; 9.

SMART; SM00355; ZnE_C2H2; 9.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; PROSITE; PS50157; ZINC_FINGER_C2H2_2; NON_TER 1
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Q8VHT8;

Q1-MAR-2002 (TrEMBLrel. 20, Created)

Q1-MAR-2002 (TrEMBLrel. 20, Last seque

Q1-JUN-2002 (TrEMBLrel. 21, Last annot

Transcription factor IIIA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                               Hanas J.S., Hocker J.R., Cheng Y.-G., Lerner M.R., Brackett Lightfoot S.A., Hanas R.J., Madhusudhan K.T., Moreland R.J., "cDNA cloning, DNA binding, and evolution of mammalian transfactor IIIA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE-21673987; PubMed-11814676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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                                                                                                                       Local S. 265;
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TGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQC
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Pred. No. 1.1e
32; Mismatches
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Pred. No. 6.4e
23; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                             7084F95B74D168BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           evolution of mammalian transcription
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                                                                                                                                     6.4e-131;
ches 42;
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; Murinae; Rat
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mambaerts P.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Mayashiraki P., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Query Match
Best Local S
Matches 167
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Q9CSW1;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2610111101Rik protein (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";

Mature 409:685-690(2001).

EMBL; AKOL1845; BABAZ7876.1; -.

HSSP; P03001; 1TF3.

MGD; MGI:1913846; Gttf3a.

InterPro; IPR000822; Znf_C2H2.

Pfam; PF00096; Zf-C2H2; 6.

PROSTIE: PS00028; ZIMC_FINGER_C2H2_1; 5.

PROSTIE: PS00028; ZIMC_FINGER_C2H2_2; 5.
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                                                                                                                                                                            DNA-binding; Zinc-finger.
NON_TER 1 1
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       Conservative
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6J; TISSUE-EMBRYO;
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77.78;
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Q9W7D7;
01-NOV-1999
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-!- COFACTOR:
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SMART; SM00355; ZnF_C2H2; 9.

PROSITE; PS00197; ZFEZS_FERREDOXIN; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.

PROSITE; PS00157; ZINC_FINGER_C2H2_1; 6.

DNA-Dinding; Iron-sulfur; Metal-binding; Zinc-finger.

DNA-Dinding; Iron-sulfur; Metal-binding; Zinc-finger.

SEQUENCE 368 AA; 42356 MW; A0A84CF04C3B144D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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InterPro; IPR000822; Znf_C2H2.
279
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CEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPP
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                                                                                                                                                                     PNFKCSNIRCTATFDSHIARKAHEKKHAGYSCPHKDCQVVEHTWSKLQRHLAK-HPVSFT
                                                                                                                                                                                                                                                                                   FQCKFANCAKSFIDAQRLKKHQNSAHGNH--KFKCNQPKCSLSFKKRRLLKLHLKEHNVH 133
                                                                                                                                                                                                                                                                                                                                                                                                   FTCTHAGCGACFPREWKLKAHETVHTGERPCACPTAGCGSLFKRTSHLKRHVLQHKGVKG 75
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Best Local S
Matches 109
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL: AL132675; CAB59689.1; -.

R EMBL: AV091590; AAM00046.1; -.

R HSSP; P07248; 1ARD.

R InterPro; IPR000822; Znf_C2H2.

R Pfam; PP00096; zf-C2H2; 10.

R ProDom; PD000003; Znf_C2H2; 1.

R PROSITE; P000003; Znf_C2H2; 1.

R SMART; SM00355; ZnF_C2H2; 9.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.

R PROSITE; PS00157; ZINC_FINGER_C2H2_1; 8.

R PROSITE; PS0157; ZINC_FINGER_C2H2_1; 8.

R PROSITE; PS0157; ZINC_FINGER_C2H2_2; 9.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.
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Q9UTL5;
01-MAY-2000
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McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSCHYDGCDAQFYTQQHLERHIE--VHRKPKPYACTWEGCDECFSKHQQLRSHISACHTH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH-QCQHTN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHCPYEECGKKYSRPSLLEQHLRTHSNERPFVCDYTGCSKAFYRKSHLKIHKRCHTNVKP
                                                                                                                   HDQKEKELSSNLVSDVAKK-IINEVTGH
                                                                                                                                                              HDPDKKKMKLKVKKSREKRSLASHLSGY
                                                                                                                                                                                                                                                                                                                                                             RETHKEEILCEVCRKTFKRKDYLKQHMKTH---APERDVCRCPREGCGRTYTTVFNLQSH 266
                                                                                                                                                                                                                                                                                                                                                                                                           LLPYPCTYQDCELRFATKQKLQNHVNRAHEKIISYSCPHESCVGHEGF--EKWSQLQNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
                                                                                                                                                                                                                ISVIHEGNMAFHCD--SCGTKFGYKHMLQRHLERGTCKKAHKPYINECGIKHDGIEGVAI
                                                                                                                                                                                                                                                              ILSFHEESRPFVCEHAGCGKTFAMKQSLTRH-----
                                                                                                                                                                                                                                                                                                             REAHVPS--CSICGRQFKTAAHLRHHVVLHQTTLEERKTYHCPMEGCKKSFTRSSALKKH
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109; Conserv
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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Pred. No. 7e-38;
B; Mismatches 1
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Q9R161;
01-MAY-2000
01-MAY-2000
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PRINTS; PR00048; ZINCFINGER. 
SMART; SM00355; ZNF_C2H2; 19
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HSSP; P08047; 1SP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     code for large proteins in vitro."; DNA Res. 4:141-150(1997).
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KIAA0326.
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                                                                                                                                                                                                                                                                                                           PY-KCPE--CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-----AKTWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTGEKPYKCTECEKAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPVVPANEPSLRELVQG-------RPAGAEKPYICN--ECGKSFSQWSKLLRHQ 227
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116; Conser
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               (TrEMBLrel.
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Primates;
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Pred. No. 7.6e-31;
2; Mismatches 11:
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Best Local Sim
Matches 115;
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R InterPro; IPR001909; KRAB.

R InterPro; IPR001909; KRAB.

R InterPro; IPR000822; Znf_C2H2.

R Pfam; pF001352; KRAB; 1.

R Pfam; pF001906; zf-C2H2; 15.

R PFINTS; PR00048; ZINCFINGER.

R PFODOm; PD000003; Znf_C2H2; 12.

R PTODOm; SM00349; KRAB; 1.

R SMART; SM00349; KRAB; 1.

R R PROSITE; PS50805; KRAB; 1.

R PROSITE; PS50805; KRAB; 1.

R PROSITE; PS50157; ZINC_FINGER_C2H2_1; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 16.
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Hauser L., York M., Shannon M., Stubbs L.;
Hauser L., York M., Shannon M., Stubbs L.;
"Differential expansion of homologous zinc-finger gene f human chromosome 19q13.2 and mouse chromosome 7.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AP167321; AAD45930.1; -.
EMBL; AP167321; AAD45930.1; -.
HSSP; P25490; 12NM.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--CGKGFSQASNLQAHQSVHTGEK---PFKCNACQKRFSQASHLQAHQRVHTGERPYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE--CGKRFSLSFNLHSHQRVHTGEKPYKCEE-CGKGFSSASSFQSHQRVHTGEKPFCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CGKGFTQRSHLQAH-ERIHTG-EKPYKCG--DCGKRFSCSSNLHTHQRVHTEEKPYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCGKGFSQSSYFQAHQRVHTGEKPY-RC--DVCGKRFNWSLNLHNH-QRVHTGERPYKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PECGKSFNQSSHLYAHLPIHTGEKPYCCD--NCGKGFSRSTDLNIHCRVHTGEKPYKCEV 372
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Pred. No. 3.
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Sciurognathi;
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thi; Muridae; Murinae; Mus.
                                                    Vertebrata;
ia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), DB 11;
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                                                       Euteleostomi;
; Pipidae;
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RESULT
Q9VXB4
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Best Local
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VXB4; PRELIMINARY;
Q9VXB4; 01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit Eukaryota; Metazoa; Arthropoda; Pterygota; Neoptera; Endopterygo
                                                                                                                                                                                                                                                                                                                                                                                                             CG9609 protein CG9609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: EMBL; U65897; AAB07010.1; HSSP; P25490; 1UBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "XFDL 141.";
Submitted (AUG-1996) to the
                                                                                                                                                                                                                                     STRAIN-BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bourguignon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTECGKSFAAKKNLKRHQMIHTGEKPHECTE--CGKQFLEKSKLKRHHLSHTGVKPFSCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VC--TECGKSFRKKCELKSHLQ--VHTGVKQFVCTECGKSFRDRSELNIHINVHTGKTFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCAATGCDQKFNTKSNLKKHFERKHENQQKQYIC----SFED-----
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107; Conserv
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eoptera; Endopterygota; Diptera; Brachyco
Drosophilidae; Drosophila.
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Last annotation updat
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Pred. No. 3
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., Kodira C.D., Krafit C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McNill X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McNill X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA McNill X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA McNill X., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA McIson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sin
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003503; AAF48663.1; -.
R EMBL; AF003503; AAF48663.1; -.
R FIYBBSE; FBgn0030787; CG9609.
R FIYBBSE; FBgn0030787; CG9609.
R InterPro; IPR000822; Znf_C2H2.
R Pfam; PF00096; Zf-C2H2; 8.
R PROSITE; PS00028; ZinC_FINGER_C2H2_1; 8.
R PROSITE; PS00028; ZINC_FINGER_C2H2_2; 7.
R DNA-Dinding; Metal-Dinding; Zinc-finger.
DNA-Dinding; Metal-Dinding; Zinc-finger.
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du
Durbin K.J., Evangelista C.C., Ferriac C., Ferriera S., Fleischma
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
    318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                         259
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KRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL
                                            YLRNLRQHMLTAH-SGRRFECQALDCGRCFSSAQNLARHLLRDHKDGATKKELKAKKKDK
                                                                                                                                                                                 T-----HKEEILCEVCRKTFKRKDYLKQHMKT---HAPERDVC-----RCPREGCGRTYT
                                                                                                                                                                                                                              EIREHTLEYPYSCSK--CSRGFYQQWQCQSHEPSCKLYEC-PGCPLQFDKWTLYTKHCRD
                                                                                                                                                                                                                                                                           QC-QHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWTELLKHVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHI-LTH---
                                                                                         TVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAV-VHDPDKKKMKLKVKKSRE
                                                                                                                                                                                                                                                                                                                        ESAAKKTVKCALEECSKMFISVSNMTRHMRETHES-PKVYPCS--QCSAKFSQKLKLKRH
                                                                                                                                                                                                                                                                                                                                                                     --TGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH
                                                                                                                                                                                                                                                                                                                                                                                                                  KYACSMPKCEATFKRLDQLDRHEYHHTGIKKHACSYEGCDKTYSIVTHLKRHLRSTHERP
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30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 406.5; DE
Pred. No. 1.5e-2
55; Mismatches 1
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)gall C.J.,
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S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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Q9Z2X6
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Best Local S
Matches 98
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Q91WM0;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                                                                                            Q9Z2X6
Q9Z2X6;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 14.
ProDom; PD000003; znf_C2H2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50805; KRAB: 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_14

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

DNA-binding; Hypothetical protein; Zinc-finger.

SEQUENCE 559 AA; 64216 MM; C08F544C0E2A429C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMEL; BC014712; AAH14712.1; InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 STRAIN-C57B6;
             SEQUENCE FROM
                                    NCBI_TaxID=10090;
                                                 Mus musculus (Mouse).

Fukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                   Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 64.2 kDa protein.
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                                                                                                                                                                                                                             501 KPYVCKQ--CGKAFTLSSSLRRHDVVHSEEK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                           SKTGEGGKTKSTSRKRRRDAGRS-----KHSRLSKLACLQL 358
                                                                                                                                                                                                                                                   RPFVCEHAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                            PYSCKLCGKAFTHSNYLQIHKRIHTGEKPYVCK----ECGKAFARSTSLHIH-EGTHSGE
                                                                                                                                                                                                                                                                                                     EILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEES
                                                                                                                                                                                                                                                                                                                               KPYVCKQ--CGKAFAQSSYLHIHQRSHTGEKPYVCKQCGKAFTRSSHLQIHK-ITHTGEK
                                                                                                                                                                                                                                                                                                                                                     PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVC-QKGCSFVAKTWTELLKHVRETHKE
                                                                                                                                                                                                                                                                                                                                                                               YVC--KHCGKAFTQSSYLRIH-KRTHTG-EKPYIC--KQCGKAFARSSHLQIHKRSHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                               YVCK--HCGKAYTTYNTLRAHERSHTGEKPYVCKH--CGKAYTSYSTLRAHERSHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 36.:
98; Conservative
                                                                                                9 (TrEMBLrel. 10,
9 (TrEMBLrel. 10,
2 (TrEMBLrel. 21,
r protein sll-6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                PRELIMINARY;
TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RETINA;
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Last annotation updat
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                                                                                                                                      Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 406.5;
Pred. No. 2.
                                                 Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Interpro; IPR007303; AAH07303.1; -.

R Interpro; IPR00199; KRAB.

R Interpro; IPR000822; Znf_C2H2.

R Pfam; PF001352; KRAB; 1.

R Pfam; PF00096; Zf-C2H2; 19.

R ProCom; PD000003; Znf_C2H2; 5.

R PROSITE; PS50805; KRAB; 1.

R PROSITE; PS50805; KRAB; 1.

R PROSITE; PS50805; KRAB; 1.

R PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50807; ZINC_FINGER_C2H2_1; UNKNOWN_18.

PROSITE; PS50807; ZINC_FINGER_C2H2_2; 19.

W DNA-binding; Zinc-finger.

DNA-binding; Zinc-finger.
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Best Local
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InterPro; IPR000822; Znf_C2H2.
Pfam; PF001352; KRAB; 1.
Pfam; PF001352; KRAB; 1.
Pfam; PF00096; Zf-C2H2; 15.
PRINTS; PR00048; ZINCFINGER.
PRODOM; PD000003; Znf_C2H2; 6.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 15.
PROSTTE; PS50805; KRAB; 1.
PROSTTE; PS50805; KRAB; 1.
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"Zinc finger protein.";
"Zinc finger protein.";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB020542; BAA34724.1; -.
                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last se
01-JUN-2002 (TrEMBLrel. 21, Last an
Similar to zhoc finger protein 224.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96IR4;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB020542; BA/
HSSP; P08047; ISP2
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q961R4
                                                                                                                                                                                                                                                           TISSUE-EYE;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVCK--HCGKAYTTYNTLRAHERSHTGEKPYVCKH--CGKAYTSYSTLRAHERSHTGEKP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPYVCKQ--CGKAFTLSSSLRRHDVVHSEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYSCKLCGKAFTHSNYLQIHKRIHTGEKPYVCK----ECGKAFARSTSLHIH-EGTHSGE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Primates;
                                                                                                                                                                                                                                                                                                                                                            Chordata;
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    Created)
    Last sequence up
    Last annotation

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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                        Craniata; Vo
Catarrhini;
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94B3416511BE9B19 CRC64;
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2.4e-29;
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                                                                                                                                                                                                                                                                                                                                          Hominidae;
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RESULT 14
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Query Match
Best Local S
Matches 104
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P70046;
P70046;
01-FEB-1997
01-FEB-1997
                                                                                             Interpro; IPR000822; Znf_C2H2.

Pfam; PF00096; zf-C2H2; 12.

PRINTS; PR00048; ZINCFINGER.

ProDom; PD000003; Znf_C2H2; 3.

SMART; SM00355; ZnF_C2H2; 12.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 12.

DNA-binding; Metal-binding; Nuclear protein; Zir SEQUENCE 411 AA; 46530 MW; E7309FEBFEFB9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: EMBL; U67077; AAB72012.1; HSSP; P25490; 1UBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=97321550; PubMed=9178260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XFDL141.
                                                                                                                                                                                                                                                                                                                                                                                                 xenopus laevis.";
Mech. Dev. 63:99-108(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene encoding two structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pieler T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bellefroid E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcription regulation and alternative splicing gene encoding two structurally distinct zinc finges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCQN-----GESP-NCVE-DKMLSTVAVLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKSFRMKIHYQVHLVVHTGEKPYKCEVCGKAFRQSSYLKIHLKAHSVQKPF-KC--EECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKTWTELLKH----VRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEGCGKHFASPSKLKRHAKAHEG --- YVCQ --- KG ----- CSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSLNLDMHQRVHTGEKPYTCGECGKHFSQASSLQL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQASHLLTHQRVHSGEK---PFKCEECGKSFSRSAHLQAHQKVHTGEKPYKCGECGKGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGFNQSSRLQIHQL-IHTGEKPYKCEECGKGFSRRADLKIHCRIHTGEKPYNCEECGKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTYTTVFNLQSHILSFHEESRPFVCEHAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
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                       20.2%;
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21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence up
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Pred. No. 2.9e-29;
                       Score 405;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouwmeester T., Rausch
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                       2e-29;
                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                  Zinc-finger
704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     finger
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                                              Length 411;
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104;

Conservative

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107;

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Best Local Simi
Matches 105;
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Q9H559;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BA526D8.4 (Novel KRAB box containing C2H2 type zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01352; KRAB; 1.

Pfam; PF00096; zf-C2H2; 17.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00349; KRAB; 1.

SMART; SM00349; KRAB; 1.

PROSITE; PS00028; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 18.

DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babbage A.;
Submilted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AL136981; CAC12728.1; -.
HSSP; P07248; IPAA.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
InterPro; IPR0019822; Znf_CC2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ILCEVCRKTEKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRP 276
                                                                                                 FKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE 216
                                                                                                                                                                                                                CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPL 161
                                                                YECSE - - CGKAFIOKSTLSMHQRIHRGEKPYVCTECGKAFFHK - - SHFITHERIHTGEKP
                                                                                                                                                                             C--TVCGKAFTDRSNLIKH--OKIHTGEKPYKCS--DCGKSFTWKSRLRIHQKCHTGERH
                                                                                                                                                                                                                                                                                                                                                     CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 101
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                                                                                                                                                                                                                                                                                             CS--DCGKSFIKKSQLHVHQRIHTGENPFIC--SECGKVFTHKTNLIIHQKIHTGERPYI 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 AA; 97660 MW; A86DCA4CDD75541D CRC64;
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Pred. No. 4.9e-29;
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Search completed: February 10, 2003, 17:47:29 Job time : 89 secs

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Maximum DB seq length: 2
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Perfect score:
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and is
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003
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              ABK45138
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,		nove	Spl	family	Human prostate exp	Human colon cancer	Human polynucleoti	Human polynucleoti	Human genome-deriv	Probe #7096 used t	used		bone n	expre			Human breast cell	cDNA encoding colo	Kidney cancer rela	Japanese medaka fe	Human ORFX polynuc	Vector TFIIIA/Zif-	Plasmid pTFIIIAZif	DNA encoding zinc	Vector TFIIIA/Zif-	Plasmid pTFIIIAZif		Nucleotide sequenc	Activated T-cell d	Human gene signatu	cDNA encoding colo	9	Human eukaryotic i	prostate ex		Human colon cancer	

ALIGNMENTS

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Human; transcription factor; htfIIIA; DNA-binding protein;
transcription; ribosomal RNA 5S gene; transcriptional control;
                                                                                                                                                                                                                          04-SEP-2000
                                                                                                                                                                                                                                           AAA15405;
Bordon-Pallier F,
                                   10-NOV-1998;
                                                     09-NOV-1999;
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                       DNA encoding a human transcription factor designated htfIIIA.
                                                                                                                                                                                                                                                            AAA15405 standard; DNA;
                 (HMRI ) HOECHST MARION ROUSSEL.
                                                                      18-MAY-2000.
                                                                                       WO200028024-A1
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                                   98FR-0014146.
                                                    99WO-FR02738
                                                                                                                          Location/Qualifiers 176..1273
                                                                                                        /*tag= a
/product= "transcription factor"
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Rocher C;
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Best Local Similarity 100.0%;
Matches 1273; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a human transcription factor designated htfIIIA. The polypeptide is probabaly a DNA-binding protein probably involved in initiating transcription of the gene for ribosomal RNA 55 and maintaining the stability of transcription of other control genes therapeutic or diagnostic compositions for diseases associated with disorders of transcriptional control, particularly cancer or other inherited diseases. The htfIIIA polynucleotide can also be used to detect anomalies in gene transcription, particularly for diagnosis of inherited disease, also for studying diseases involving hTFIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1273
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CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
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                                              CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
                                                           CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
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                                                                                                        ACGCAAACATGAAAATCAACAAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGAC
                                                                                                                                          CAAGCACACGGGGGAGAGCCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCAT
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DB; AAY93317.
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                                                                                                                                                                                                                                                                                                                                                                Human; ss; granulocytic cell; DNA chip; bacterial infection viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosi cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel distress crohn's disease; ulcerative collitis; periodontal disease;
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                                                                              03-OCT-2000;
                                                                                                                                                                                                                                                                                                                                        granulocyte activation; chronic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in granulocytic cells #221
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Weissman

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CC (GCA), by detecting the level of expression of gene(s) (GS) activation (CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CD DNA chip analysis as given in the specification and comparing CC DNA chip analysis as given in the specification and comparing CC GC, where differential expression of GS is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent CC characterial the expression of at least one gene in GS; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a filammatory disease, by detecting the CC chronic of expression in a sample of the tissue of gene(s) from GS, where CC the level of expression in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response is a subject to a pathogen or flammation with an agent that modulates the expression of gene(s) from GS, M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for detecting GCA; M2 is useful for consistency disease, capacity capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening GCA; M3 is useful for screening GCA; M3 is useful for capacity for many for the propo
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                                                                                          The sequence encodes human transcription factor-IIIA (hTFIIIA), a constant with 9 zinc finger domains, which is necessary for the initiation of 55 RNA gene transcription, binding to an internal control region of the 55 gene. The coding region control region of the 55 gene. The coding region of the gene has been isolated from a human foetal brain cDNA library (Claimed) is given in ANT14037. A fragment lacking a 5'-portion of the gene has been isolated by complementary to the gene has been isolated from a human foetal brain cDNA library (OTK7-1), and the 5'-portion of the gene has been isolated by complementary to Hil-E (AAT14040), Hil-H (AAT14041) and AP-2 (AAT14042), complementary to anchor primer AAT14043. Reverse transcription using H-11R is followed by anchor primer ligation and PCR using AP-2 and Hil-E, to give a full-length cDNA, OTK7. The gene and its encoded protein may be used in diagnosis, identification or therapy of hereditary diseases such as cancer, or other diseases resulting from abnormal transcriptional control, and to analyse the mechanisms involved in
                                             Query Match
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The sequence encodes human transcription factor-IIIA (hTFIIIA),

a DNA binding protein with 9 zinc finger domains, which is necessary

for the initiation of 5S RNA gene transcription, binding to an

internal control region of the 5S gene. A fuller cDNA sequence

with flanking regions is given in AAT1403B. A fragment lacking a

5'-portion of the gene has been isolated from a human foetal brain

cDNA library (OTK7-1), and the 5'-portion of the gene has been

isolated by 5'-rapid amplification of cDNA ends using primers H11-R

(AAT14039), H11-E (AAT14040), H11-H (AAT14041) and AP-2 (AAT14042),

complementary to anchor primer AAT14043. Reverse transcription using

H-11R is followed by anchor primer ligation and PCR using AP-2 and

H11-E, to give a full-length cDNA, OTK7. The gene and its encoded

protein may be used in diagnosis, identification or therapy of

hereditary diseases such as cancer, or other diseases resulting from
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                 The present sequence represents a fragment of a human transcription factor (designated htfIIA) gene. The polypeptide is probabaly a DNA-binding protein probably involved in initiating transcription of the gene for ribosomal RNA 5s and maintaining the stability of transcription of other control genes. The htfIIIA polynucleotides and polypeptides are used to make therapeutic or diagnostic compositions for diseases associated with disorders of transcriptional control, particularly cancer or other inherited diseases. The htfIIIA polynucleotide can also be used to detect anomalies in gene transcription, particularly for diagnosis of inherited disease, also for studying diseases involving hTFIIIA.
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                                                              AAGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAA
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TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
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                                                                                       cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic
useful f
                    present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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03-NOV-1999;
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colorectal carcinoma;
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ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndro PCOS; ovarian cyst; dysmenorrhees; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiblody preparation; cytostatic; immunomodulatory; chromosome 13q12.3-13
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                                                                                                                                                                       Claim 1;
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                                                                                                                                 invention relates to 2175 novel human ovarian antigens (ABP41054-
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DB; ABP41846.
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                                                                                                                                                                       SEQ
                                                                                                                                                                                                                     nucleic acid molecules encoding novel ovarian polypeptides, n the prevention, treatment and diagnosis of cancer (e.g. cancer), immune disorders, cardiovascular disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chiamydia, HIV, toxoplasmosis, and toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic toxic t
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Matches 419; Conserv
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ABK44450-ABK46237 represent coding sequences of human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                           1094
                                                                                                                                                                                                                                                                                                                                                                     proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification b
                                                                                                                                                                                                                                                                                                                                   Sequence
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            AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAAGGGAGTTTGGCCTCTCATCTCAGT
                                                                                                                       CGCTGTCCAAGAGGAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAAGCCAT
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                                                                  ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTTTGTACATGATCCTGACAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Η;
                                                                                                                                                                                                                                                                                                    DB 24; Length 439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic;
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                                                                                Query Match
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Matches 418;
                                                                                                                                                                                                   The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46237 represent coding sequences of human colon tumour proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1154
                                                                                                                                                               for this supplied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-223283P
28-MAR-2001; 2001US-279763P
29-JUN-2001; 2001US-302051P
                                                                                                                                                                                                                                                                                                                                                                                                  New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK45138 standard; cDNA; 439
                                                                                                                                       Sequence
                                                                                                                                                                                         Note: With the exception of SEQ ID No 1 and 2, the sequence data
                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001; 2001WO-US24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunotherapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                   914 CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCAAAGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GE,
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                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon tumour;
                                                                                           Similarity
                                                                                                                                       439
                                                                                                                                                               patent did not form part of the printed specification but was by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 689; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meagher MJ,
                                                                                Conservative
                                                                                                                                    BP; 141 A; 99 C; 93 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon
                                                                                          32.7%;
99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
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                                                                              Score 416.8; DB 24;
Pred. No. 8.3e-99;
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                                                                                                           DB 24;
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABB60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid that is differentially expressed in tissues useful for determining the presence of colon cancer in or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2000; 2000US-237271P
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer related nucleotide sequence SEQ ID NO:3194.
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RESULT 11
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding gene resides, and in tissue profiling, forensics, analysis, mapping and diagnostic applications. (I) can be used antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                         Human
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                                 Schlegel R,
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                                                                                                                                                                                                                     WO200160860-A2
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                                                                                                                                                                     20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       662 AAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                            482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAAACATGG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGTGGCAAAACA-TTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGAACTTCTGAAACATGTGAGAGAAAACCCCATAAAGAGGGAAATACTATGTGAAGTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAGGTCCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGTGGCAAAACATTTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCAAAGCCATATCCTCCTTCCATGAGGAAAGCCCGCCTTTTTNGTGTGAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGATGTATGTCGCTGTCCAAGANAAGGCTGTGGAAGAACCTAT-CAACTGTGTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402;
                                                                                                                                                                                                                                                                                                       prostate expression marker cDNA 49222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                          MILLENNIUM PREDICTIVE MEDICINE
                                                                                ; 2000US-183319P.
; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-2119007P.
; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                 Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 196 A; 116 C; 106 G; 117 T; 2 other;
                                                                                                                                                                     2001WO-US05171
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                     marker;
                                                                                                                                                                                                                                                                                                                                                                                cDNA;
                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.4%;
96.6%;
                                                                                                                                                                                                                                                                    gene;
                                                                                                                                                                                                                                                                                                                                                                                466
                                  Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 374; DB; Pred. No. 1.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
..4e-87;
                                                                                                                                                                                                                                                                                 pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076
                                                                                                                                                                                                                                                                                                                                                                                                                                            537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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WPI; 2001-662795/76

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RESULT 12
ABV19459
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                              Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                   1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patien (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                         13-SEP-2002
                                                                                                                                                                                                                                                  ABV19459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                               23-AUG-2001
                                                           WO200160860-A2
                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer in a patient;
  20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient;
                                                                                                                                                                                                                                                                                                                        464
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATGCCGGGAAAACATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA 796
                                                                                                                                                                                                                                                                                                                        TTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302;
                                                                                                                                                           prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466
                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9624; 11750pp;
                                                                                                                                                           expression marker cDNA 19450
                                                                                                                   marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
                                                                                                                                                                                                                                                CDNA;
                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
                                                                                                              cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmacodyanamic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 301.4; DB 2
Pred. No. 1.2e-68;
                                                                                                                                                                                                                                               ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ი</u>
                                                                                                                             carcinogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmacogenomic marker
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                                                                                                                             pharmacodyanamic marker;
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                                                                                                                                                                                                                                                                                                                                                                                                       1036
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RESULT 13
AAH22129/
ID AAH2
XX
AC AAH2
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the cc specification or its complement. (I) is useful for:

Cc (a) assessing whether a patient is afflicted with prostate cancer;

Cc (b) monitoring the progression of prostate cancer in a patient;

Cc (c) assessing the efficacy of a test compound to inhibit prostate

Cc cancer in a patient;

Cc (d) assessing the efficacy of a therapy for inhibiting prostate cancer

in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient

(h) assessing the aggressivence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
              AAH22129
                                         129/c
AAH22129 standard;
                                                                                                                                            1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient;
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                                                                                                                424
                                                                                                                                                                        364
                                                                                                                                                                                                   977
                                                                                                                                                                                                                              304
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                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is also useful as a
                                                                                                                                                                     1=
                                                                                                                                           TT
                                                                                                                                                                                                                                             TGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                                                             CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAAACATTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                    GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA
                                                                                                                                                                                                                             TGTCCAAGAGAAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               301;
                                                                                                                                            1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 3184; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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99.7%;
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); Mismatches
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                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 T;
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RESULT 14
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Best Local
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heIF3;
                                                                                                                                                                                                                                                 1208
                                                                                                                                                                                                                                                                                                                                                                                                                            1401
                                                                                                                                                                                                                                                                                                                                                         1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a human eukaryotic initiation factor (eIF) designated heIF3), which is expressed in human dendritic cells. heIF3 has translation initiation factor activity. Also described in the present invention are methods for the preparation and detection of the heIF3 protein and nucleotide sequences. The present sequence encodes heIF3, as given in the present invention.
                   AAS73534;
                                                                                                                                                                                                                                                                                                                                                                                           1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human translation initiation factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-282654/30
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                                                      AAS73534 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1401 BP; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2000; 2000CN-0116791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2000; 2000CN-0116791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local L
246;
                                                                                                                                                                                                                                   GGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACCTTACCCTT
                                                                                                                                                                                                                                                                                                      CTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAAC
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                                                                                                                                                                                                                                                                                                                                                       AAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAACGGAGTTTGGCCTCTCAT
                                                                                                                                                                                                                                                                                                                                                                       AAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAACGGAGTTTGGCCCTCTCAT
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                                                                                                                                           GGCTAA
                                                                                                                                                                            GGCTAA 1273
                                                                                                                                                                                                               GGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 17 (disclosure);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                    CDNA; 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%; Score 246; DB 22; 100.0%; Pred. No. 5.7e-54;
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AAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAGAAAATGAAGCTC

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The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC art from wino but was obtained in electronic format directly from WIPO CC art from wino in the printed contractions obtained in electronic format directly from WIPO case of the printed of the sequences of the sequences.
                  Query Match
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 9338; 103pp; English.
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23-AUG-2000; 2000US-0649167
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                                                                           Sequence 1889 BP; 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
Local Similarity es 275; Conserv
                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss
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                  18.5%;
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Score 236; DB 23;
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Matches 234
                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46237 represent coding sequences of human colon tumour
                                                                                                                                                                                               proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 610; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2001; 2001WO-US24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding colon tumour protein,
                                                                                                                                                                        Sequence
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239 GTGGAAGACAAAATGCTCTCGGCAGTTCCAGTACTTACCCTTGGCTAA 286
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nes 234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               the progression of cancer -
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                                                                                                                Conservative
                                                                                                            18.4%; Score 234; DB 24; Length 234; 100.0%; Pred. No. 3.3e-51; ative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spirite REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
LENGTH: 1906
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ALIGNMENTS

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1814)..(1814)
; OTHER INFORMATION: n is a,
US-09-724-676-44689
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Best Local Similarity
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RESULT 2
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; Sequence 44689, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
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NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version
SEQ ID NO 44689
LENGTH: 1906
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1814)..(1814)
OTHER INFORMATION: n is a,
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                                             TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
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NOS: 97222
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RESULT 3
Sequence 44634 App
GENERAL INFORMATION
GENERAL INFORMATION
FILE OF INVENTION
FILE REFERENCE: 1
CURRENT APPLICATIC
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NUMBER OF SEQ ID I
SOFTWARE: PatentII
SEQ ID NO 44634
LENGTH: 2019
TYPE: DNA
ORGANISM: HOMO SE
FEATURE:
NAME/KEY: misc_fe
LOCATION: (1927)
COTHER INFORMATION
US-09-724-676-44634
                                                                                                                                                                                                                                             Sequence 44634, Application US/09724676
(GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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                                               ACGTGTCTCGGCACGTGGCAGCGCCCTGGCCCTTGGAGGCGCCCCGGGA
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RESULT 4

US-09-724-676A-44634
; Sequence 44634, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative spl
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44634
LENGTH: 2019
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: TYPE: DNA
: ORGANISM: Homo sapiens
: PEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1927). (1927)
: OTHER INFORMATION: n is a.c.g. o
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEO ID NO 44445
LENGTH: 2104
                                                                                                                                                                                                                                                                               Sequence 44645, Application US/09724676 GENERAL INFORMATION:
                                                                                                              Best Local Similarity Matches 1270; Conservat
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Best Local
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                                                                                                               Conservative
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                                                                                                              Score 1268.2;
Pred. No. 0;
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                                      CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
                                                                               TCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGC
                                                                                                                       TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
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; ORGANISM: Homo sapiens
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US-09-724-676A-44645
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LENGTH: 2104
TYPE: DNA
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
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                                     CTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTG
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44678
LENGTH: 2239
TYPE: DNA
ORGANISM: Homo sapiens
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TCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACT
                                  CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
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; APPLICANT: Compugen LTD;
; TITLE OF INVENTION: Variants of alternative splicing;
; TITLE OF INVENTION: Variants of alternative splicing;
; TITLE OF INVENTION: Variants of alternative splicing;
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28;
; CURRENT FILING DATE: 2000-11-28;
; NUMBER OF SEQ ID NOS: 97222;
; SOFTWARE: Patentin version 3.2;
; SEQ ID NO 44678;
; LENGTH: 2239;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-44678
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                         CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
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Sequence 44656, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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US-09-724-676A-44656
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GENERAL INFORMATION
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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Sequence 44623, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44623
LENGTH: 2352
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 4462; Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEO ID NO 44632
LENGTH: 2352
TYPE: DUA
ORGANISM: Homo sapiens
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44601
LENGTH: 2384
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-44601
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TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44601
LENGTH: 2384
TYPE: DNA
ORGANISM: Homo sapiens
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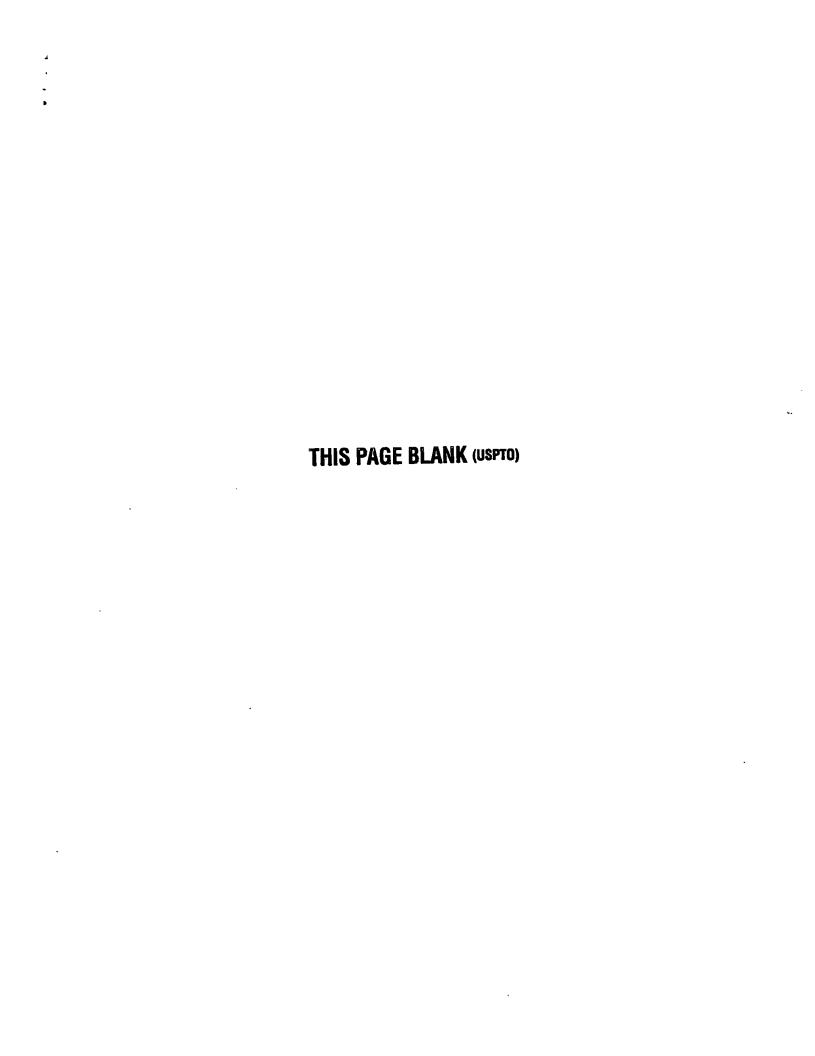
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RESULT 15
US-09-724-676-44667
Sequence 44667, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: VARIANTS of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIMS DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44667
LENGTH: 2536
TYPE: DNA
ORGANISM: Homo sapiens
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Minimum Maximum Post-processing: Minimum Match Maximum Match Listing first š Total number of hits satisfying chosen parameters: Scoring table: Sequence: Title: Perfect score: Searched: nucleic 9 2: DB seq length: 0
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Gapop 10.0 , Gapext 1.0 February 10, 2003, 12:48:16; 2054640 seqs, 14551402878 residues atgcgcagcagcggccga.....cagtacttacccttggctaa 1273 0% 100% 45 summaries ; Search time 3381.18 Seconds
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SUMMARIES

Result No. 000 a 000 0.0 a O 0.0 11233 .2 11088 .8 11088 .8 919 .2 9889 .8 889 .8 470 .2 47 Query Match 439 3 163421 3 197709 3 1694709 3 106141 3 200885 3 200885 3 1693 4 1518 4 131 5 131 1 171065 1 123905 1 171705 1381 1399 1173 1098 1920 1298 1971 996 97979 193126 11722 206622 Length DΒ HSU14134 AF391799 AF391798 BC032929 AC00474390 AC0016444 AL353741 AX396111 AX396111 AX396111 AX396111 AX396111 AX396111 AX396111 AX396111 AX1611 AX16111 AX16111 AX16111 AX16111 AX16111 AX1611 AX1611 AX16111 AX16111 AX16111 AX1611 Ħ AK057993 Homo sapi AF391799 Mus muscu AF391799 Mus muscu AF391799 Mus muscu AF391799 Mus muscu AF391799 Mus muscu AF391799 Mus muscu AF2016414 Homo sapi AC006045 Homo sapi AC074390 Homo sapi AC073641 Homo sapi AC013644 Homo sapi AC013641 Homo sapi AC013641 Homo sapi AC0137659 Human DNA AF265440 Homo sapi AC1137059 Human DNA AC0112400 Homo sapi AC1137659 Arenopus bor M32472 X.borealis X58369 R.plpiens m M85211 Rana pipien AC116311 Homo sapi AC113317 Homo sapi AC113317 Homo sapi AC113318 Homo sapi AC113717 Homo sapi AC11371 Homo sapi AC11371 Homo sapi AC11371 Homo sapi AC11371 Homo sapi AC11371 Homo sapi AC113758 B.americanu AC117566 B.americanu AC117569 B.americanu AC117569 B.americanu AC121881 Mus muscu AX396395 Sequence AC124828 Mus muscu AX3053174 Sequence AX053174 Sequence AX053170 Sequence AX053171 Sequence AX053173 Sequence D32257 Human GTF3A E10962 cDNA's enco U20272 Human DNA/R U14134 Human trans Description

ALIGNMENTS

MIIIA 1	
CUS	HUMIIIA 1381 bp mRNA linear PRI 07-FEB-1999
EFINITION	nscription factor
	complete cds.
CESSION	D32257
ERSION	D32257.1 GI:1000446
EYWORDS	GTF3A; Xenopus transcription factor IIIA homologue.
URCE	Homo sapiens cDNA to mRNA, clone_lib:librarry of T.Fujiwara, S.Shin
	and Y.Nakamura clone:39H11.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SFERENCE	1 (bases 1 to 1381)
AUTHORS	Arakawa,H., Nagase,H., Hayashi,N., Ogawa,M., Nagata,M.,

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                                                         CAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCAT
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Tel: 03-3918-0111 (ex. 4501), Fax: 03-3918-0342)

Location/Qualifiers
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Molecular cloning, characterizati
novel human gene (GTF3A) that is
transcription factor IIIA
Cytogenet. Cell Genet. 70 (3-4),
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FVCEHAGGGXTFAMKQSLTRHAVVHDDDKKKMKLKVKKSREKREFGLSSQWIYPPKRK
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/clone="39H11"
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CDNA'S encoding hTFIII/

E10962

E10962.1 GI:22028822

JP 1996070870-A/1.
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Verte Eukaryota; Metazoa; Chordata; Catarrhini; Hon 1 (bases 1 to 1399) [1] (bases 1 to 1399) [1] (bases 1 to 1399) [1] (bases 1 to 1399) [1] (bases 1 to 1399) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (bases 1 to 1396) [1] (ba
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omo sapiens (human)
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                                                                                                              Drew,P.D., Nagle,J.W.,
Becker,K.G.
                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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             2 (bases 1 to 1173)
Becker, K.G.
Direct Submission
Submitted (25-JAN-1995) Kevin G. Becker,
Diseases and Stroke/NIH, Neuroimmunology
Pike, Bethesda, MD 20892, USA
Pike, Docation/Qualifiers
1. .1173
∕organism*"Homo
                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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partial cds.
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CGCAAACATGAAAATCAACAAAAACAATATATGCAGTTTTGAAGACTGTAAGAAGACC
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                                                               GCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGAA
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<1...1092
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484 . .5
/note=",
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649 . .7
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829. .895
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736. .805
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VCRKTFKRKDYLKQHMKTHAPERDYCRCPREGCGRTYTTVFNLQSHILSFHEESRPFV
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208. .
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118. .184
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Accession Number P03001"
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283 c 265 g 262 t
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                                                                      Cloning and
Unpublished
                                                                                                                                                                                Human transcription factor U14134 U14134.1 GI:551534
          Submitted (29-AUG-1994) Kevin G. Becker Neurological Diseases and Stroke/NIH, Nackville Pike, Bethesda, MD 20892, USA
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1098)
                                         Direct Submission
                                                   Becker, K.G.
                                                                                            Drew, P.D., Nagle, J.W.,
Becker, K.G.
                                                                                                                                                  Homo sapiens
                                                             (bases 1 to
Location/Qualifiers
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                                                                                   expression
                                                                                   analysis
                                                                                                       Canning, R.D.,
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                    Becker, National Institute
/NIH, Neuroimmunology Branch
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                                                                                    human TFIIIA
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                    AAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATC
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339
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661. 732
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/note="encodes zinc-finger"
754. 822
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/note="encodes z
574. .636
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CRCPREGCGRTYTTVFNLQSHILSFHEESRPFYCEHAGCGKTFAMKOSLTRHAVVHDP
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/note="encodes zinc-finger"
208. .276
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394. 462
/gene="HTFIIA"
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/db_xref*"taxon:9606"
/clone="C2H2-34"
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263 c 244 g 252 t
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490. .558
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IIIA, Swiss-Prot Accession Number p03001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="2 yr old female"
/tissue_type="brain"
/clone_lib="Human hippocampus cDNA library, Stratagene
Number_936205"
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Pred. No. 1.7e-190;
D; Mismatches 8;
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REFERENCE

ORGANISM

Homo sapiens clone:STM05057.

Eutheria;

Chordata; Primates;

R to mRNA,

clone_lib:STM

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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                                            AKUD/993 1920 bp
Homo sapiens cDNA FLJ25264 fis,
TRANSCRIPTION FACTOR IIIA.
Oligo capping; fis (full insert Homo sapiens stomach mucosa cDNA
                        AK057993.1 GI:16553988
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                                                           mRNA linear PRI 31-OCT-2001 clone STM05057, highly similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugano, S. and Suzuki, Y. Direct Submission (24-ocr-2001) Sumio Sugano, Institute of Medical Submitted (24-ocr-2001) Sumio Sugano, Institute of Medical University of Tokyo, Laboratory of Genome Structure, Human Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Ja (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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/db_xref="taxon:9606"
/clone="STM05057"
/tissue_type="stomach mucosa"
/clone_lib="STM"
/note="cloning vector: pME18SFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                 of Oklahoma Health Science Cooklahoma City, OK 73104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-JUN-2001) Biochemistry/Molecular Biology, University of Oklahoma Health Science Center, 800 Research Parkway, Suite 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \label{eq:lightfoot}  \textbf{Lightfoot}, \textbf{S.A., Hanas}, \textbf{R.J., Maduhadson}, \textbf{K. and Direct Submission} 
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Hanas, J.S., Hocker, J.R.,
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/product="transcription factor IIIA"
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                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 GTTGTACATGATCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAA
                                              TGTGAACATGCTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCT
                                                                                           ACTGTGTTTAATCTCCAAAGCCATATCCTCTCCTTCCATGAGGAAAGCCGCCCTTTTGTG
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HDPDKKRMKLKVRAPRERRSLASRLSGYFPPKRKQEPDYSLPNASAESSSSPEAQLPP
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2 (bases 1 to 1071)
4 Hanas, J.S., Hocker, J.R., Lerner, M.R., Brackett, D.J.,
4 Hanas, J.S., Hocker, J.R., Maduhadson, K. and Moreland, R.J.
Lightfoot, S.A., Hanas, R.J., Maduhadson, K. and Moreland, R.J.
Direct Submission
Direct Submission
Submitted (14-JUN-2001) Biochemistry/Molecular Biology, University
Submitted (14-JUN-2001) Biochemistry/Molecular Barkway, Suite 448,
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Rodentia;
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                                                             Score 691; DB pred. No. 1.3e 0; Mismatches
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No. 1.3e-140;
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han, K.T. and Moreland, R.
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                                                                                                                                                                                                                       681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: National Institutes of Health Intramura

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.llr Series: IRAK Plate: 65 Row: 1 Column: 4
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
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Gene Collection (MGC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
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Contact: MGC help desk
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Mammalia; Eutheria;
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/translation="mcKtwtelkhnreahkeditcnvcormfkrrdylkohmkthap/translation="mcKtwtelkhnreahkeditcnvcormfkrrdylkoslmrhsv
erdvyrcprogocgrtytvfnloshilsfheekrpfvcehagggktfankoslmrhsv
vhdpdkkrmklkvraprerrslasrlsgyfpdkrkqepdyslpnasaesssspeaqlp
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old mouse. Taken by biopsy."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="general transcription
/protein_id="AAH32292.1"
/db_xref="GI:21595508"
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/db_xref="taxon:10090"
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78.9%;
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                                                         Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Department of Genetics,
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Direct Submission

Direct Submission

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Submitted (03 FEB-2000) Department of Genetics,

Submitted (03 FEB-2000) Department of Genetics,

University, 4444 Forest Park Avenue, St. Louis,
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                                                                                                                                                                                                                         Waterston, R.
Center project name: H_DJ0531G15
                                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                       Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                        4444 Forest Park Avenue,
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                                                                                                            Sequencing
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. problems,

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc and

SOURCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION: The actual start of this clone is at base position 1 actual end is at base position 97979 of RP4-53IG15. 6:84-9 (1994). The library is from one male donor. details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc. This clone was derived from human PAC library RPCI-4, prepared Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Joannou et al., Nature Genetics (http://www.genomesystems.com). PCYPAC2 of RP4-531G15; For further prepared bу

This clone contains STS_sWSS2758 (NID:gl113567)

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VERSION KEYWORDS SOURCE ORGANISM REFERENCE ACCESSION DEFINITION Locus AC074390/c AUTHORS TITLE JOURNAL Eukaryota; Metazoa; Chordata; Cri Mammalia; Eutheria; Primates; Ca 1 (bases 1 to 111722) Sulston, J.E. and Waterston, R. Toward a complete human genome si Genome Res. 8 (11), 1097-1108 (1) AC074390 Homo sapiens AC074390 Homo sapiens AC074390.6 Homo sapiens 111722 bp BAC clone RP11-515K14 Craniata; Vertebrata; Catarrhini; Hominidae; (1998) from 7, Hominidae; complete Linear Euteleostomi; 21-FEB-2002

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send
                                                      NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTD-2105K18, 2000 bp overlap; the clone sequenced to the right is RP11-533K11, 2000 bp overlap actual start of this clone is at base position 141753 of CTD-2105K18; actual end is at base position 16029 of RP11-533K11
                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Submitted (19-JAN-2002) Genome
University School of Medicine,
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        Polymorphisms
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The sequence of Homo sapiens BAC clone RP11-515K14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mailto:egreen@nhgri.nih.gov ,
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Contact: sapiens@watson.wustl.edu
----- Summary Statistlcs
Center project name: H_NH0515K14
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                                                         actual end is at base position 16829 of RP11-533K11.
have been identified between AC016444 and AC074390
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Submitted (26-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced gi:6778507.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                 Direct Submission
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Birren, B., Linton, L.,
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Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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* This record will be updated with the finished sequence.
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Sequenciny vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 190829 bases at least Q40
Consensus quality: 190829 bases at least Q30
Consensus quality: 202013 bases at least Q20
Insert size: 213000; aggrose-fp
Insert size: 205122; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved
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13493 13592: gap of 100 bp
13593 14758: contig of 1166 bp in length
14759 14858: gap of 100 bp
14859 16187: contig of 1329 bp in length
16188 16287: gap of 100 bp
16288 18628: contig of 2341 bp in length
18629 18728: gap of 100 bp
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18629 2545: contig of 3817 bp in length
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80935 102411: contig of 21477 bp in length

102412 102511: gap of 100 bp

102512 177924: contig of 25413 bp in length

127925 128024: gap of 100 bp

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GAGAGAAACCCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAACGCAA 861
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                                                                                                                                                                TGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 741
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                                                                                                                          TGGGAAGCATTTTTCCCCATCCATCCAGC-----AAGCGGCAAGGCCCATGCGGGCTC
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

The problem of the course of the course databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jan 28, 2001 this sequence version replaced gi:12580980.
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                            Em:, EMBİ; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                        http://www.sanger.ac.uk/HGP/Chr9
RP11-575C20 is from the library RPCI-11.2 constructed
of Pieter de Jong. For further details see
                                                                                        VECTOR: pBACe3.6
This sequence is
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AL353741.16
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                                                                                                                         http://www.chori.org/bacpac/home.htm
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                                                  end of clone RP11-279El is at right end of clone RP11-21817
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∕organism≖"Homo sapiens"
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TGGACGGAACTTCTGAAACATGTGAG----AGAAACCCATAAAGAGGAAATACTATGTGA
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RESULT 15
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods
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AL550467 AL550467
AL555777 AL555777
BM562682 AGENCOURT
AL574318 AL574318
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1968 row: o column: 07
High quality sequence stop: 673.
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BM553401
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGG
                                                                                                                            GTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCA
                                                                                                                                                                      AGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATTCAAGT
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5 adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
01 a 276 c 275 g 223 t 3 others
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_41"
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KEYWORDS
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AUTHORS
TITLE
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 GCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTA--CATGA 1080
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                                GAAGGTTCACCAGGGAGCCGTGGGCCGGGCGCGCGGTTCCCGGCACGTGTCTCGGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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AL518337 LTI_NFL011_NBC1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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all: segref@genoscope.cns.fr, Web : www.genoscope.cns.
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                                                                                                                                                                           270
                                                                                              Conservative
                                                                                                                                                                 /note-"organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-cligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fulllength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="neuroblastoma cells"
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                                                                                                                                                                                                                                                                                                                                                                                                /sex≖"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Pred. No. 2.8e-191;
6; Mismatches 6;
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AL555777
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Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRY cedex - F7
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1 (bases 1 to 881)
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AL555777
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                                                                                  Conservative
                                                                                                                                  /Clone="CSODK002YJ18"
//Clone_lib="LTI_NFL006_PL2"
//Lissue_type="placenta"
//Lissue_type="placenta"
//note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Pive prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Location/Qualifiers
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/db_xref="taxon:9606"
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braries and nor
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5', mRNA sequence.
BM562682
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1059)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                          Homo sapiens
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                                                                                                     human
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Homo
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="organ: brain: Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
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/Tissue_type="placenta"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the NotI and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
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                                                                                                                                                                                                a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8: Email: fliang@lifetech.com URL:
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2478 row: j column: 20
High quality sequence stop: 636.
Location/Qualifiers
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National Institutes of Health, Mammalian
Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACCAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

16 a 212 c 200 g 201 t 1 others
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Full-length cDNA libraries and no Unpublished (2001)
                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 957)
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                  segref@genoscope.cns.fr,
                                                 /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL:
                               http://fulllength.invitrogen.com"
240 c 227 g 206 t
                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC024YE05"
                                                                                                                                                                                /clone_lib_"LTI_NFL003_NBC3"
                                                                                                                                                                        /sex="male"
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                                                                                                                                                              /tissue_type="neuroblastoma cells"
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AL574698 LTI_NFL006_PL2 H
Prime, mRNA sequence.
AL574698
AL574698.1 GI:12935148
L1.W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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/clone_tib="LTI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
bttp://fillloss.bt.doublecom.url

Email: filang@lifetech.com URL:
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AGENCOURT_6439143 NIH_MGC_71
5', mRNA sequence.
BM541851
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1111)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                       Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                     BM541851.1
EST.
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REFERENCE AUTHORS TITLE KEYWORDS SOURCE FEATURES COMMENT DEFINITION cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at: http://image.lni.gov e column: 08 High quality sequence stop: 654. //b xref "taxon: 9606"
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//clone=lib="NIH_MGC.71"
//Lissue_type="leiomyosarcoma"
//tissue_type="leiomyosarcoma"
//lab_host="DH10B (phage-resistant)"
//note="Organ: uterus; vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. " /organism="Homo sapiens" information can

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HRI human cDNA project; 5'- & 3'-end one
Research Institute; cDNA library constru
Virology, Institute of Medical Science,
Helix Research Institute.
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Genomics Laboratory
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1532-3 Yana, Kisarazu, Cl
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Pred. No. 2.9e-174;
0; Mismatches 4;
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l Science, University of Tok
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                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MCC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 902)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
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BQ644275.1 GI:21768447
EST.
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AGENCOURT_8355851 NIH_MGC_100
5', mRNA sequence.
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Plate: LLCMX484 row: j column:
High quality sequence stop: 642.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6885421"
/clone=lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="D+10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-d" priming. Directionally cloned
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
301 a 208 c 197 g 194 t 2 others

GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT GTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAACATTTTG GCAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCA 419 GGACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTAT ATGCCAAGGCCCACGAGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACAT CCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTAT GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT CCTCTCATCTCAGTGGATATAT-CCCTCCCAAAAGGAAACAAGGGCAAGG ATCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGAGTTTGG CTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATG GCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAG TCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGAC AACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGA GC-ANCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCA GGACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTAT TCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGAC al Similarity 875; Conserv Conservative 86 59 3.3%; 0 Score Pred. Mismatches 836; No. 4. DB 14; 1.5e-173; nes 12; Length Indels 902; 1188 Gaps 539 1019 479 599 1079 189 848 729 669 959 609 899 549 839 489 779 429 719 369 659 309 249 70 359 ω

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              TGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGGAAATAC
                                                                                                                                ATGAACCTCTATTCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCA
                                                                                                                                                                                                AGCCGTTTGTTGTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGA 527
                                                                                 GCAAGGCCTTCATCA-GGACTACCATCTGAGCCGCCACATTCTMACTCACACAGGAGAAA 875
                                                               AGCCGTTTGTTTGTGCAGCCAATGGCTGATCAAAAATTCAACACAAAATCAAAACTTGA 815
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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AL578193
AL578193.1 GI:12942034
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//db_xref="taxon.9606"
//clone="CSODKO02YJ18"
//clone="CSODKO02YJ18"
//clone=lib="LTI_NFLO06.PL2"
//tissue_type="placenta"
//note="Yector: pcMySPORT 6; Site_1: NotI: 1st strand cDNA
//note="Vector: pcMySPORT 6; Site_1: NotI: 1st strand cDNA
//note="Vector: pcMySPORT 6; Site_1: NotI: 1st strand cDNA
//note="Vector: placenta"
//note="vector with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: fllang@llfetech.com URL:
http://fulllength.invitrogen.com"
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98.5%;
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Pred. No. 8.3e-172;
4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence
BQ278693
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                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LICM2044 row: f column: 22
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                      quality sequence stop: 610.
Location/Qualifiers
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: poTB7; Site_1: EcoR
Site_2: XhoI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXhoI sites using
following 5' adaptor: GGCACGAG(G). Library const
                                                                                             /clone="IMAGE:5805333"
/clone_lib="NIH_MGC_107"
                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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              TCCAAAGCCATATC--
                                      GTATGTCCCCTGTCCCAAAAGAAGGTTGTGGAAAAAACCTATTCCACTGTGGGTTAATCC
                                                  GTATGTCGC--TGTCCAAGAGAAGGCTGTGG-AAGAACCTATACTGCTGT--GTTTAATC
                                                                                                     ATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCAT--GCCCCCAGAAAGGGAT
                                                                                                                                                        TCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAAC
                                                                                                                                                                                             CCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACT
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                                                                                         ATTTTAACGCCAAGATTACCTTAAGCCACCCATGAAAAACTCTTGGCCCCAGAAAGGGAT
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Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1810 row: d column: 07

High quality sequence stop: 880.

Location/Qualiflers
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           GCGCTTCCCCAGGAGGTTCATCTGCCTCCCTTCCCTGACTGCAGCGCCAATTACAGCAAAAGCC
                                                                                           ACCATCGCCGACGCGTTCATTGCAGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCCGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg,
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Similarity 98.6%;
08; Conservative
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/tissue_type="epithelioid carcinoma cell line"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTBF; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORIXhoI sites using the
following 5' adaptor: GCCACGGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/db_xref="taxon:9606"
/clone="IMAGE:4906710"
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ch com	992	933 840	874 781	817 721	758 661	698	638 541	578 481	518 421	458 361	398 301	338 241
Search completed: February 10, 2003, 17:44:07 Job time : 2015.41 secs	GAAAGCCGCCTTTTGTGTGT 1012	GTGGAAGAACCTATACTACTGTGTTTAAT-CTCCAAAGCCATATCCTCTCCTTCCATGAG 991 	GCAACACATGAAAACTCATGCCCCAGAAAGGGATGTATGT	AGAGGAAATACTATGTG-AAGTATGCCGGAAAA-CATTTAAACGCAAAGA-TTACCTTAA 873 	TGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCAT-AA 816 	TCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTATGTATG	CAGCATACCAATGAACCTCTATTCAAGTGTACCCAGGAAGGA	AGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGC 637 	TCAAACTTGAAGAAACATTTTGAACGCAAACATGAAAATCAACAAAAACAATATATAT	ACAGGAGAAAAGCCGTTTGTTGTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAA 517 	GAAGGGTGTGGCAAGGCCTTCATCAGGGACTACCATCTGAGCGGCACATTCTGACTCAC 457 	TGGAAGCTTGACGCGCACCTGTGCAAGCACACGCGGGGAGAGACCATTTGTTTG



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//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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GENERAL INFORMATION:

APPLICANT: King, Gordon E.

APPLICANT: King, Madeleine Joy

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heather

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SED ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 326

LENGTH: 439
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Best Local Similarity 99.8%;
Matches 419; Conservative
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Pred. No. 8.4e-103;
0; Mismatches 1;
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APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANC
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTMARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 439
RESULT 3
US-09-920-300A-689
; Sequence 689, Application US/09920300A
; Patent No. US20020136728A1
; GERAL INFORMATION:
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APPLICANT: Meagher, Madelelie U.,
APPLICANT: Weigher, Madelelie U.,
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT APPLICATION ONBER: US/09/920,300A
CURRENT FALING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FASCEQ FOR Windows Version 4.0
SEQ ID NO 689
LENGTH: 439
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-920-300A-689

32.7%; Score 416.8; DB 10;
                                                                                                                                                                                                                                                                                                                                                                       US-10-033-528-689
                                  US-10-033-528-689
                                                 SEQ ID NO 689
LENGTH: 439
TYPE: DNA
ORGANISM: Homo:
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Best Local Similarity
Matches 418; Conserv
                                                                                                                                                                                    APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Su, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF COLON C
FILE REFERENCE: 210121.547C1
                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
                                                                                                                        SOFTWARE: FastSEQ for Windows Version
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99.5%;
32.7%;
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Pred. No. 2.3e-102;
0; Mismatches 2;
Score 416
.8
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BB
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Length 439;
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2071-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
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PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
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PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,3416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,378
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                                          NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4064
                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-08
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                                                                                                                                 2000-08-07
                                                                           Windows Version
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER

FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FASCSEQ FOR Windows Version 4.0

SEQ ID NO 610

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RESULT 7
US-10-033-528-610
US-10-033-528-610; Sequence 610, Application US/10033528; Patent NO. US20020131971A1; GENERAL INFORMATION:
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APPLICANT: Meagher, Madel
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heath
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hes 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 18.4%; Score 234; DB 10; Local Similarity 100.0%; Pred. No. 1.9e-53; hes 234; Conservative 0; Mismatches 0;
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 610
LENGTH: 234
                                                                                                                                                                                                                                                              APPLICANT: Burmer, Glenna C.

APPLICANT: Brown, Joseph P.

APPLICANT: LifeSpan BioSciences, Inc.

TITLE OF INVENTION: Nucleic Acid Sequences and TITLE OF INVENTION: Nucleic Acid Sequences and TITLE OF INVENTION: Associated With Aging File Reference: 017473-0011100 With Aging CURRENT APPLICATION NUMBER: US/09/292.758

CURRENT FILING DATE: 1999-04-14

EARLIER APPLICATION NUMBER: US 60/081,887

EARLIER APPLICATION NUMBER: US 60/081,887

EARLIER FILING DATE: 1998-04-15

NUMBER OF SEO ID NOS: 147

SOFTWARE: FastSEQ for Windows Version 3.0

SEO ID NO 68

LENGTH: 362
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Sequence 68, Application US/09292758
Publication No. US20020197602A1
GENERAL INFORMATION:
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                                                                                                                                          Query Match 17.8
Best Local Similarity 96.7
Matches 263; Conservative
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Best Local Similarity
Matches 234; Conserv
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96.7%;
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Pred. No. 3.5e-51;
0; Mismatches 5;
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Pred. No. 1.9e-53;
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GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: ULLMAN, Christopher G.
TITLE OF INVENTION: GENE SWITCHSS
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/09/995,973
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 947
TYPE: DNA
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US-09-995-973-2
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US-09-995-973-2
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Best Local Similarity 57.6%;
Matches 273; Conservative
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CCGCTTTTCTCGCTCGGATGAGCTTACCCGCCATATCCGCATCCACACACGCCA 499
                                     ACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 741
                                                                           TCATCAGTTCAGTCACACACAGCAGCTGCCGTATGCTTGCCCTGTCGAGTCCTGCGATCG
                                                                                                              ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAAT 627
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Pred. No. 3.6e-31;
0; Mismatches 201;
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RESULT 11
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CURRENT FILING DATE: 200-12-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
                   Sequence 1, Application US/09995973
Publication NO. US20030024006A1
GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: ULLMAN, Christopher G.
APPLICANT: ULLMAN, Christopher G.
TITLE OF INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/09/995,973
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APPLICANT: Yen Choo, et al.
APPLICANT: Yen Choo, et al.
APPLICANT: Yen Choo, et al.
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       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (723)..(908)
OTHER INFORMATION: transactivation domain of VP64, o
OTHER INFORMATION: listed below) same as SEQ ID NO:
NAME/KEY: misc_feature
LOCATION: (909)..(938)
OTHER INFORMATION: c-myc tag, other features except
OTHER INFORMATION: ted above) same as SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE;
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TYPE: DNA
ORGANISM: Artificial Sequence
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les 273; Conserv
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       2002-03-19
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Pred. No. 3.6e-31;
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US-09-995-973-1
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US-09-732-348-4
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 995
TYPE: DNA
ORGANISM: Artificial S
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yen Cho
NAME/KEY: misc_feature
LOCAPION: (15)..(17)
OTHER INFORMATION: translational ir
NAME/KEY: misc_feature
LOCAPION: (16)..(416)
OTHER INFORMATION: Fingers 1 to 4 c
NAME/KEY: misc_feature
LOCAPION: (308)..(416)
                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09732348 Patent No. US20020046419A1
                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 4
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Best Local :
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CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FILE REFERENCE: 6
                                                                                                                                                         LENGTH: 99
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al Similarity 57.6%;
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ON: Regulated Gene Expression 674538-2001
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NAME/KEY: misc_feature
LOCATION: (417)..(689)
OTHER INFORMATION: three fingers of zinc f
NAME/KEY: misc_feature
LOCATION: (701)..(722)
OTHER INFORMATION: Nuclear Localization Si
NAME/KEY: misc_feature
LOCATION: (957)..(986)
                                  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5443
LENGTH: 449
                                                                                                                                                                                                                                                                                 Sequence 5443, Application Patent No. US20020110850A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 273; Conserv
                                                                            CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILLING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                             APPLICANT: L1, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                      APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, Willia
ORGANISM: Homo sapiens
                       TYPE: DNA
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Pred. No. 3.7e-31;
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Best Local :
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OTHER INFORMATION: n e
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                                                                TNCNTTGTGGGCAAAAACTGGGACGGGACTTCTGNAACTGTGAGNGAAACCCTTAAGGGG
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                                                                                        TCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAG
                                                                                                                                                                                                                                                                 -GAAGACCTTTAAGAAA-----CATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAA 648
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Pred. No. 1.9e-28;
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Indels Length

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302 703 242

449; 17;

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1111)
; OTHER INFORMATION: n = A,T,C
US-09-833-381-1175
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Sequence 1747, Application US/09920300A
Patent No. US20020136728A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 223, 323
OTHER INFORMATION: n = A
IS-09-920-300A-1747
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APPLICANT: Robison, Keith E.
APPLICANT: RObison, Keith E.
TITLE OF INVENTION: No. US2002013Z090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1747
LENGTH: 368
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Best Local Similarity 61.1%;
Matches 140; Conservative
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SEQ ID NO 1175
LENGTH: 1111
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                                                                                                                                                                                                                                                                                                  APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                        A,T,C or
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Pred. No. 1.9e-13;
0; Mismatches 89; Indels 0;
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Search completed: February 10, 2003, 12:58:32 Job time: 81.105 secs
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Best Local Similarity
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                                                                                                            356 GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGNCAAAAACATGGACGGAACTTCTGAAA 297
                                                                                                                      737 GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA 796
                                                      296 CATGTGAGAGAAACCCATAAAG
                                                                                797 CATGTGAGAGAAACCCATAAAG
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98.8%;
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                                                      275
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                                                                                                                                                                                .1e-12;
                                                                                                                                                                                          Length 368
                                                                                                                                                                 Indels
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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6: /cgn2_6/ptodata/1,
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     atgcgcagcagcggcgcga.....cagtacttacccttggctaa 1273
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                DB
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            US-08-523-376-2
US-08-523-376-1
US-09-492-985-1
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US-09-34-323-5
US-08-570-227A-1
US-09-07-991-1
US-08-92-463-14
US-09-07-843-3
US-09-907-843-3
US-08-946-241B-1
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US-08-9428-1
US-08-044-045-1
US-08-044-083-1
US-08-233-609-1
US-08-244-083-1
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US-08-444-745-1
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7401.927 Million cell updates/sec
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                                      ; NAME/KEY: CDS
; LOCATION: 20..1288
; IDENTIFICATION METHOD:
US-08-523-376-2
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Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                       FEATURE:
                                                                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                            IMMEDIATE SOURCE:
LIBRARY: human
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2100 Penr
CITY: Washington
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Kouichi, OZAKI
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Satoshi, TAKEDA
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Sequence 13, App	Sequence 3, Appl.	Sequence 3, Appl.	Sequence 3, Appl	Sequence 20, App.	Sequence 7, Appl.	Sequence 7, Appl.	Sequence 7, Appli	Sequence 4, Appl	Sequence 1, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 1, Appl	Sequence 1, Appli	Sequence 1, Appl:

ALIGNMENTS

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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1399 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sadahito, SIN
TITLE OF INVENTION: hffilia Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/523,376
FILING DATE:
                                                                                                                                                                                    : human fetal brain cDNA OTK7
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Score 1231.6; DB 1; Pred. No. 3.9e-312;
                     Length 1399;
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Matches
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TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
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                                                                                                       CCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGA
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APPLICATION: 536
FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEFAX: (202) 293-7860
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-523-376-1
96.58
99.48
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US-08-523-376-1
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                                                                                                                                                                         Matches 1264;
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2100 Pennsylvania Avenue,
CITY: Washington
STATE: D.C.
COUNTRY: United States
COUNTRY: United FORM:
LEP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
OPERATING SYSTEM: PC-005/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: YOShikazu, SHIMADA
APPLICANT: KOUIChi, OZAKI
APPLICANT: Sadahito, SIN
TITLE OF INVENTION: hTFIIIA GENE
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                121
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                                              GTGCCGGCGTCGCGCGAAGGTTCAGCAGGGAGCCGTGGGCCGGGGGGGCGCG-CGGTTCCCCGGC
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2100 Pennsylvania Avenue,
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99.4%;
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Pred. No. 2.3e-311;
0; Mismatches 4;
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                                              CCTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGT
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   GTCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTAC
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                                     CCTCTCATCTCAGTGGATATAT-CCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGT
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APPLICANT: Song, An M.
APPLICANT: Chen, Ya-Fen
APPLICANT: Chen, Ya-Fen
APPLICANT: Krensky, Alan M.
TITLE OF INVENTION: RFLAT-1: A Transcription Fa
TITLE OF INVENTION: Activates RANTES Gene Expre
FILE REFERENCE: SUN-113P
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT EILING DATE: 2000-01-27
EARLIER APPLICATION UMBER: 60/117,576
EARLIER FILING DATE: 1999-01-27
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                                                                                       Sequence 1, Application Patent No. 6376240 GENERAL INFORMATION:
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; LENGTH: 1471
; TYPE: DNA
; ORGANISM: mouse
US-09-492-985-11
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APPLICANT: Chen, Ya-Fen
APPLICANT: Krensky, Alan M.
APPLICANT: Krensky, Alan M.
TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
TITLE OF INVENTION: Activates RANTES Gene Expression
FILE REFERENCE: SUN-113P
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,576
FEARLIER FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-492-985-11
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Matches 170;
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                       CTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT
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70; Conservative
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48.9%; Pred. No. 4.2e-07;
vative 0; Mismatches 178;
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US/09492985

Expression

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Sequence 3. Application US/09362123A
Patent NO. 6451558
GENERAL INFORMATION:
APPLICANT: Cooke, Michael Paul
APPLICANT: Sitenko, Oksana
TITLE OF INVENTION: NO. 6451558el Genes in the
FILE REFERENCE: 4-30629A/SYS
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US/09/362,123A
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 09/128,310
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LEUGTH: 2992
                                                                                          ; NAME/KEY: CDS
; LOCATION: (82)..(1710)
US-09-362-123A-3
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Query Match
Best Local Similarity
Matches 142; Conserv
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Best Local Similarity 48.9%;
Matches 193; Conservation
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1430
TYPE: DNA
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TTCAGCAGGGAGCCGTGGGCCGGGCGCGCGCTTCCCGGCACGTGTCTCGGCACGTGGCA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTCGGTGTCGTCCTTGACCATCGCCGACGCGTTCATTGCAGCCGGCGAGAGCTCAGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCCCCCAGCCCGGCGTGGAGCGAGCCGGAGCCCGAGGCGGGGCTGGAGCCCGAGCGG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTTCGCCTGCAGCTGGCAGGACTGCAACAAGAAGTTCGCGCGCTCCGACGAGCTGGCG 1023
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            Conservative
                             54.68;
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            0
          Score 58.8; DB 4;
Pred. No. 8e-06;
0; Mismatches 112;
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Pred. No. 1.2e-06;
0; Mismatches 201; Indels 1
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                                                Length 2992;
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US-08-570-227A-1
Sequence 1, Application US/08570227A
Patent No. 5981217
GENERAL INFORMATION:
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Zic 1 Protein gene; Genbank Acession D76435
US-09-234-332-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cedars-Sinal Medical Center
APPLICANT: Michel F. Levesque, M.D.
APPLICANT: Toomas Neuman, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF
FILE REFERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
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APPLICANT:
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                                                                                                                                                              1822 GACCGCAAGAAGCA 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                               521 AACTTGAAGAAACA 534
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Local Similarity 55.2%;
les 107; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCAAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAAGGGTGTGGCAAGGCCTT 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAGCCGGCGAGAGCTCCAGCTCCGACCCCGCGCGCCCCGCGCTTCCCAGGAGGTTCAT
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Subramaniam,
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Pred. No. 9.1e-05;
0; Mismatches 87; Indels
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EPIDERMAL CELLS
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Sequence 1, Application US/09077991
Patent No. 6207375
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T.C.
APPLICANT: Roche, P.C.
TITLE OF INVENTION: TGF-Beta inducib
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
FILE
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REFERENCE/DOCKET NUMBER: 15(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                     1365
                                                                                                                                                                                                                                                                                                                                                      1245
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MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: DAA ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE E
TITLE OF INVENTION: BY OSTEOBLASTS
                                                                                                                                                                                                                                                                                                                                                                                                                  1185 AGGAGTCACATCTGTAGCCACCCAGGATGTGGCAAGACATACTTTAAAAGTTCCCCATCTG 1244
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                    467 AAGCCGTTTGTTTG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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REFERENCE:
                                                                                                                                                                                                                     AAGAAATTTGCGTG 1378
                                                                                                                                                                                                                                                                                                                   GGCAAGGCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAA 466
                                                                                                                                                                                                                                                                                                                                                    AAGGCCCACACGAGGACACACACAGGAGAAAAGCCTTTCAGCTGTAGCTGGAAAGGTTGT
                                                                                                                                                                                                                                                                                  GAAAGGAGGTTTGCCCCGTTCTGATGAACTGTCCAGACACAGGCGAACCCACACGGGTGAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106;
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ION: (TIEF-1)
150.157US2
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            TGF-Beta inducible early factor-1 (TIEF-1) and a method to detect b
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Pred. No. 0.00023;
0; Mismatches 88
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               detect breast cancer
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-077-991-1
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GENERAL IN
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Matches 106;
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CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: PCT/US96/19555
EARLIER FILING DATE: 1996-12-11
EARLIER APPLICATION NUMBER: US 08/570,227
EARLIER FILING DATE: 1995-12-11
       APPLICATION NUMBER: US/07/935, FILING DATE: APPLICATION NUMBER: EP 91 114 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 3047 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOM
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTT 346
                                                                                                                                                                                                                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                               FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAAATTTGCGTG
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Similarity 54.6%;
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1800 Diagonal Road
                                                                                                                                                                                                                                                                                                                                                                                                  USA
(703)683-4109
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                                                                                                                                           EP 91 114 300.6
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Pred. No. 0.00023;
0; Mismatches 88
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                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (79)...(3399)
US-09-657-042A-3
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-1
US-08-232-463-14
                                                             Best Loc
Matches
                                                                                       Query Match
                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 3600
                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09657042A Patent No. 6329203 GENERAL INFORMATION:
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                                                                                                                                                                                                                                         FILE REFERENCE: RTS-0148
CURRENT APPLICATION NUMBER: US/09/657,042A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 88
                                                                                                                                                                                                                                                                                                   APPLICANT: C. Frank Beni APPLICANT: Jacqueline Wyatt TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID
                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 7218 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    811 CCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCT 870
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                                                          Local Similarity
mes 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 4.1%; Score 52.8; DB 1; Length 7218;
Local Similarity 4.5%; Pred. No. 0.00043;
nes 18; Conservative 218; Mismatches 160; Indels 0
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STRANDEDNESS: single
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                                                          Conservative
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                                                                        4.1%;
51.2%;
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                                                                                                                                                                                                                                                                                                          ANTISENSE MODULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14:
                                                          Score 52.6; DB 4;
Pred. No. 0.00036;
0; Mismatches 139;
                                                                                                                                                                                                                                                                                                          GLIOMA-ASSOCIATED ONCOGENE-1 EXPRES
                                                                                       Length 3600;
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; Sequence 1, Application US/08946241B
Patent No. 5928941
; GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA NULTy, Megan M.
TITLE OF INVENTION: REPRESSOR KRUP
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            RESULT 12
US-08-946-241B-1
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US-09-907-843-3
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LENGTH: 4960
TYPE: DNA
ORGANISM: Homo s
FEATURE:
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Patent No. 6440739
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0279
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Best Local Similarity
Matches 136; Conserv
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CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                  1289
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                                                                                                                                                                                                                                                                  ATCCCAGGCTGCACCAAGA 1307
                                                                                                                                                                                                                                                                                                          TTTGAAGACTGTAAGAAGA 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGAGAAGCCATATGTGTGTGAGCACGAGGGCTGCAACAAAGCCTTCTCCAACGCCTCG 1231
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                                                KRUPPEL-LIKE FACTOR
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STREET: 22.

225 Franklin Street

Fish & Richardson P.C.

ADDRESSEE:

COUNTRY:

USA

MA

COMPUTER:

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Sequence 8, Application US/08946241B
Patent No. 5928941
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA' Nully, Megan M.
TITLE OF INVENTION: REPRESSOR KRUP,
NUMBER OF SEQUENCES: 13
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COMPUTER: IBM CONIDERCY
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,241B
FILLING DATE: 07-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,035
FILLING DATE: 05-0V-1996
APPLICATION NUMBER: 60/027,521
FILLING DATE: 07-OCT-1996
APPLICATION NUMBER: 60/027,521
FILLING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                   US-08-946-241B-8
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                   1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAAACACACGGGGCACCGCCCGTT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                     415 CTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCCGTT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                        355 CCTGTGCAAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAAGGGTGTGGCAAGGC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 CATCTGCTCCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                    COUNTRY: USA
ZIP: 02110-2804
                                                                   STATE: MA
                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Creason, Gary L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99;
                                                                                   Boston
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EDNESS: single
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Diskette
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                                                                                                                                                                     REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
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RESULT 14
US-09-309-053-1
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PRIOR APPLICATION NUMBER: 60/030,035
APPLICATION NUMBER: 60/027,521
APPLICATION NUMBER: 60/027,521
APPLICATION NUMBER: 60/027,521
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09309053 Patent No. 6077933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: MCA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5970
                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCCGTT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                    ADDAL STREET: L. STREET: MA
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
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TELEFAX: DI.
TEX: 200154
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                                                                                                                                                                                                                                 ADDRESSEE: Fish & KICHALUSH
STREET: 225 Franklin Street
APPLICATION NUMBER:
                                                APPLICATION NUMBER:
                                                                                                    OPERATING SYSTEM:
                                                                                                                      COMPUTER:
                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                IBM Compatible
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55.0%;
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                                                  US/09/309,053
08/946,241
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APPLICATION NUMBER: 60/027,521
APPLICATION NUMBER: 60/027,521

APPLICATION NUMBER:

07-OCT-1997

60/030,035

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US-09-309-053-8
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; LOCATION:
US-09-309-053-1
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09309053
Patent No. 6077933
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Lee, Mu-En
APPLICANT: MCA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 99; Conserv
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/946,241
FILING DATE: 07-OCT-1997
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCGTT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                     STREET: 225 F
CITY: Boston
STATE: MA
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                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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Search completed: February 10, 2003, 12:47:09 Job time: 111.743 secs
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US-09-309-053-8
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
                                                                      1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCCGTT 1773
                                                                                                                                                                                                                1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
                                                                                                                                         415 CTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 474
                                                                                                                                                              355 CCTGTGCAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGC 414
                                                                                                                                                                                                                                                  295 CATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCCAAAGCCTGGAAGCTTGACGCGCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
                                                                                                                                                                                                                                                                                     99;
                                                                                                                                                                                                                                                                                                      h 4.0%;
Similarity 55.0%;
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                                                                                                                                                                                                                                                                                                                       DB 3;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Pending_Patents_NA_Main:*

1: cgn2_6/ptodata/1/pna/US06_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
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7: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
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12: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
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19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.

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Query Match Length

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60.8	77.3	93.3	93.3	94.7	94.7	95.2	95.2	96.0	97.9	99.7	99.7	99.7	99.7	99.7	99.7	99.7	100.0	100.0	100.0	100.0
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RESULT 1
US-09-831-426-1
US-09-831-426-1
Sequence 1, Application US/09831426
GENERAL INFORMATION:
APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htfillA gene and c.
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 1
LENGTH: 1273
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (176)...(1270)
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: Sequence 3, Application US/09831426
: GENERAL INFORMATION:
: APPLICANT: Hoechst Marion Roussel
: APPLICANT: Bordon-Pallier, F.
: APPLICANT: Rocher, C.
: TITLE OF INVENTION: Human htFIIIA gene and coded htFIIIA protein
: FILE REFERENCE: 146.1364
: CURRENT APPLICATION NUMBER: US/09/831,426
: CURRENT APPLICATION STED ID NOS: 10
: SOFTWARE: Patentin Vers. 2.0
: SOFTWARE: Patentin Vers. 2.0
: SEQ ID NO 3
: LENGTH: 1273
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Pred. No. 1.9e-279;
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; TYPE: DNA; ORGANISM: Human; PEATURE; PEATURE; NAME/KEY: CDS; LOCATION: (176)...(1270) US-09-831-426C-1
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APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
TITLE OF INVENTION: Human htFIIIA gene and cc
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 1
LENGTH: 1273
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Matches 1273; Conserv
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Pred. No. 1.9e-279;
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APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIIA gene and co-
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SOFTWARE: DAA
CORGANISM: Human
TYPE: DNA
ORGANISM: Human
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377 360 317 300 257 240

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Sequence 9602, Application US/09644868
GENERAL INFORMATION:
APPLICANT: Holtzman, David
APPLICANT: Holtzman, Douglas A.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID N
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1168-001
CURRENT APPLICATION NUMBER: US/09/644,866
CURRENT APPLICATION NUMBER: 60,7151,063
PRIOR APPLICATION NUMBER: 50,7151,063
PRIOR FILING DATE: 199-08-27
NUMBER OF SEQ ID NOS: 10075
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 9602
LENGTH: 1597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n - A,T,C or G
US-09-644-868-9602
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                                     ACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGAC
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: LENGTH: 1597
; TYPE: DNA
; ORGANIAM: HOMO sapiens
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1597)
; OTHER INFORMATION: n = A
US-09-652-126-8862
                                                                                                                                                                                                                                                                                                                                              Sequence 8862, Application US/09652126
GENERAL INFORMATION:
APPLICANT: Shylan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1185-001
CURRENT APPLICATION NUMBER: US/09/652,126
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,132
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10051
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 8862
LENGTH: 1597
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US-09-652-126-8862
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CTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTG
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RESULT 7

US-09-652-814-10703

Sequence 10703, Application US/09652814

Sequence 10703, Application US/09652814

GENERAL INFORMATION: Douglas A.

FILLE OF INVENTION: NOVEL NUCLEIC ACID PRIVE OF INVENTION: THEREFOR THILE REFERENCE: 1600.1191-001

CURRENT APPLICATION NUMBER: US/09/652,814

CURRENT FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/152,109
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PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 10797
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 10703
LENGTH: 1597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n - A,T,C of
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        GACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGGAAATACTATGTGAAGTATG
                              TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
                                                                CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1597)
; OTHER INFORMATION: n =
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PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 2933
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1934
LENGTH: 1597
TYPE: DNA
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Matches
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2043-001
CURRENT APPLICATION NUMBER: US/09/716,
CURRENT FILING DATE: 200-11-20
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                                                   TCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGC
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; ORGANISM: Homo sapiens ; FEATURE; NAME/KEY: misc_feature LOCATION: (1)...(1597); OTHER INFORMATION: n = AUS-09-716-990-1322
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APPLICANT: Holtzman, Douglas A.
APPLICANT: HOLTZman, Douglas A.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600,2039-001
CURRENT APPLICATION NUMBER: US/09/716,990
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/166,926
PRIOR FILING DATE: 1999-11-22
NUMBER OF SEQ ID NOS: 1691
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1322
LENGTH: 1597
TYPE: DNA
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Sequence 6336, Application US/09721589
GEMERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Villeval, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID I
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600, 2045-001
CURRENT APPLICATION NUMBER: US/09/721,58:
CURRENT APPLICATION NUMBER: 00/167,380
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEO ID NOS: 7017
SOFTMARE: FastSEQ for Windows Version 4
SEQ ID NO 6336
LENGTH: 1597
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                                        LENGTH: 1597
TYPE: DNA
ORGANISM: Homo
 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n =
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Best Local Similarity
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99.8%;
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Pred. No. 1.1e
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ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature LOCATION: (1)...(1597)
OTHER INFORMATION: n = A US-09-726-788-6896
                                                                                                                                                                                                                                                                                                                                                         Sequence 6896, Application US/09726788

GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Geating, David P.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLEC
TITLE OF INVENTION: NUMBER: US/09/726,788
FILE REFERENCE: 1600.2051-001
CURRENT APPLICATION NUMBER: US/09/726,788
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,131
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 7691
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6896
LENGTH: 1597
TYPE: DNA
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Best Local Similarity
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CTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTG
                                           AGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCGCGCCCCCGCGCTTCCCAGGAGGTTCATCTG
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RESULT 12
US-60-324-185-16829
(Sequence 16829, Application US/60324185; GENERAL INFORMATION:
APPLICANT: Morris, MacDonald; APPLICANT: Lal, Preeti

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; OTHER INFORMATION: Incyte ID ; NAME/KEY: unsure ; LOCATION: 2351 ; OTHER INFORMATION: a, t, c, g US-60-324-185-16829
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Best Local :
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CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 16829
LENGTH: 2519
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Matches 1270; Conserv
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TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMORPHISMS EQUENCE DATABASES, AND SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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                                                        ; NAME/KEY: unsure
; LOCATION: 1504, 150
; OTHER INFORMATION:
US-60-172-373-18068
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                                                                                                                                                                              APPLICANT: MORTIS, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms U:
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide !
FILE REFERENCE: GX-0006 P
CURRENT APPLICATION NUMBER: US/60/172,373
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772
SOFTWARE: PERL PROGRAM
SEQ ID NO 18068
LENGTH: 1527
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                            Sequence 18068, Application US/60172373 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 1269; Conserv
                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Inc
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APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIIA gene and c
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426
CURRENT FILLING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 4
LENGTH: 1213
TYPE: DNA
ORGANISM: Human
US-09-831-426-4
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US-09-831-426-4
; Sequence 4, Application US/09831426
; GENERAL INFORMATION:
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Best Local Similarity
Matches 1212; Conserv
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                                     ATGATCCTGACAAGAAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGAGTT
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1261 TACCCTTGGCTAA 1273 ||||||||||||||||| 1201 TACCCTTGGCTAA 1213 ò

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Search completed: February 10, 2003, 14:48:16 Job time : 3133.12 secs